

FORM PTO-1390
(REV 10-95)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1787

U.S. APPLICATION NO. (If known, see 37 CFR §1.5)

09/674266

INTERNATIONAL APPLICATION NO

PCT/DE99/01258

INTERNATIONAL FILING DATE

19 APRIL 1999

PRIORITY DATE CLAIMED

28 APRIL 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES OBTAINED FROM PANCREAS TUMOR TISSUE

APPLICANT(S) FOR DO/EO/US

SPECHT, Thomas, et al.

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
 - ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
 - ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
 - ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
 - ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
 - ☒ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
 - ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
 8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
 9. ☐ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
 10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).
- Items 11. to 16. below concern document(s) or information included:**
11. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
 12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.
 13. ☐ A FIRST preliminary amendment.
 - ☐ A SECOND or SUBSEQUENT preliminary amendment.
 14. ☐ A substitute specification.
 15. ☐ A change of power of attorney and/or address letter.
 16. ☒ Other items or information:

PAPER COPY OF SEQUENCE LISTING WITH DISKETTE

U.S. APPLICATION NO (if known, see 37 CFR §1.5) 09/674266		INTERNATIONAL APPLICATION NO PCT/DE99/01258		ATTORNEY'S DOCKET NUMBER SCH 1787	
17. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)): Search Report has been prepared by the EPO or JPO..... \$860.00 International preliminary examination fee paid to USPTO (37 CFR §1.482)..... \$690.00 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$710.00 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO..... \$1000.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$100.00 ENTER APPROPRIATE BASIC FEE AMOUNT =				CALCULATIONS PTO USE ONLY	
Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	38 - 20 =	18	x \$ 18.00	\$324.00	
Independent claims	3 - 3 =	0	x \$ 80.00	\$0.00	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 270.00		
TOTAL OF ABOVE CALCULATIONS =				\$1,184.00	
Reduction of 1/2 for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).					
SUBTOTAL =				\$1,184.00	
Processing fee of \$130.00 for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
TOTAL NATIONAL FEE =				\$1,184.00	
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.					
TOTAL FEES ENCLOSED =				\$1,184.00	
				Amount to be refunded:	
				charged:	
a. <input checked="" type="checkbox"/> A check in the amount of <u>\$1,184.00</u> to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$_____ to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed.					
NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.					
SEND ALL CORRESPONDENCE TO:					
MILLEN, WHITE, ZELANO & BRANIGAN, P.C. Arlington Courthouse Plaza I 2200 Clarendon Boulevard, Suite 1400 Arlington, Virginia 22201 (703) 243-6333					
Filed: 30 OCTOBER 2000					
AJZ:jmm					
				SIGNATURE	
				Anthony J. Zelano	
				NAME	
				27,969	
				REGISTRATION NUMBER	

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

#6

Atty. Docket No: ALBRE 3

In re patent application of

SPECHT, THOMAS et al.

Serial No. 09/674,266

Filed: October 30, 2000

For: HUMAN NUCLEIC ACID SEQUENCES FROM PANCREAS TUMOR TISSUE

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

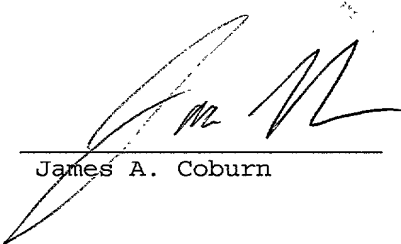
In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

Dec. 18, 2001
Date


James A. Coburn

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IN THE UNITED STATES DESIGNATED/ELECTED OFFICE

International Application No. : PCT/DE99/01258
International Filing Date : 19 APRIL 1999
Priority Date(s) Claimed : 28 APRIL 1998
Applicant(s) (DO/EO/US) : SPECHT, Thomas, et al.

Title: HUMAN NUCLEIC ACID SEQUENCES FROM PANCREAS TUMOR TISSUE

PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, D.C. 20231

SIR:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

IN THE CLAIMS:

- Claim 3, line 1, after "597-617" insert --of Claim 2--;
- Claim 4, line 3, after "597-617", insert --of Claim 2--;
- Claim 5, line 2, delete "claims 1 to 4" and insert --Claim 1--;
- Claim 6, line 1, delete "claims 1 to 4" and insert --Claim 1--;
- Claim 8, line 1, delete "claims 1 to 7" and insert --Claim 2--;
- Claim 9, line 1, delete "claims 1 to 7" and insert --Claim 2--;
- Claim 10, lines 1 and 2, delete "one of claims 1 to 9" and insert --Claim 2--;
- Claim 11, line 2, delete "one of claims 1 to 9" and insert --Claim 2--;
- Claim 13, lines 1 and 2, delete "one of claims 11 and 12" and insert --Claim 11--;
- Claim 14, lines 1 and 2, delete "claims 1 to 10" and insert --Claim 2--;
- Claim 16, line 3, delete "one of claims 1 to 10" and insert --Claim 2--;
- Claim 18, line 1, delete "one of claims 16 or 17" and insert --Claim 16--;
- Claim 19, line 2, delete "claims 16 to 18" and insert --Claim 16--;
- Claim 20, line 3, after "597-617" insert --of Claim 2--;

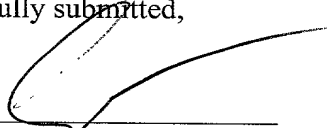
Claim 27, line 2, after "618-659" insert --of Claim 23--;
Claim 28, line 2, after "597-617" insert --of Claim 2--;
Claim 29, line 2, after "597-617" insert --of Claim 2--;
Claim 30, line 2, after "618-659" insert --of Claim 23--;
Claim 31, line 2, after "618-659" insert --of Claim 23--;
Claim 32, line 2, after "618-659" insert --of Claim 23--;
Claim 33, line 1, delete "claims 1 to 10" and insert --Claim 2--;
Claim 34, line 1, delete "claims 1 to 10" and insert --Claim 2--;
Claim 35, line 4, after "597-617" insert --of Claim 2--;
Claim 38, line 1, delete "claims 1 to 7" and insert --Claim 2--.

8. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in [claims 1 to 6] claim 2, in such a sufficient amount that they hybridize with the sequences according to [claims 1 to 6] claim 2 or a sequence having 90% homology thereto.

REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Respectfully submitted,



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09/674266

WO 99/55858

PCT/DE99/01258

Human Nucleic Acid Sequences from Pancreas Tumor Tissue

The invention relates to human nucleic acid sequences from pancreas tumor tissue, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer is the pancreas tumor, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead

to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in such a case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined

into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-157 and 597-617, which play a role as candidate genes in the pancreas tumor, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-88, 90-96, 98-120, 123-140, 142-144, and 597-617 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-88, 90-96, 98-120, 123-140, 142-144, and 597-617,
 - b) an allelic variation of the nucleic acid sequences named under a)
- or
- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-88, 90-96, 98-120, 123-140, 142-144, and 597-617 or a complementary or

allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-157 and 597-617, which are expressed elevated in the pancreas tumor tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-157 and 597-617.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-157 and 597-617 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia),
2. eukaryotic,

such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as *E. coli* or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols Seq. ID Nos. 158-596 and 618-659.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID Nos. 158-596 and 618-659 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-157 and 597-617 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 158-596 and 618-659 according to the invention can also be used as tools for finding active ingredients against the pancreas tumor, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-157 and 597-617 for expression of polypeptides, which can be used as tools for finding active ingredients against the pancreas tumor.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 158-596 and 618-659 as pharmaceutical agents in the gene therapy for treatment of the pancreas tumor or for the production of a pharmaceutical agent for treatment of the pancreas tumor.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 158-596 and 618-659.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained

from cDNAs of sequences Seq. ID Nos. 1-157 and 597-617, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-157 and 597-617, genomic BAC-, PAC- and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-157 and 597-617 for use as vehicles for gene transfer.

Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

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The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for Tumor-related Candidate Genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the pancreas tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2

Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1 Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 17 was found, which occurs 13.3 x more

strongly in the normal pancreas tumor tissue than in normal pancreas tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 17

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

In an analogous procedure, the following Northernblots were also found:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0117	0.0026	4.5763	0.2185
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0010	0.7200	1.3890
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 2

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0041	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 3

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0019	0.0000	undef	0.0000	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0063	0.0000	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0221	0.0000	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0076	0.0000	undef	0.0000	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000				
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0087				
White blood cells	0.0000				
Cervix					

		FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000		Breast 0.0000
Gastrointestinal	0.0000		Ovary_n 0.0000
Brain	0.0000		Ovary_t 0.0101
Hematopoietic	0.0000		Endocrine tissue 0.0000
Skin	0.0000		Fetal 0.0012
Hepatic	0.0000		Gastrointestinal 0.0000
Heart-blood vessels	0.0000		Hematopoietic 0.0057
Lung	0.0000		Skin-muscle 0.0032
Suprarenal gland	0.0000		Testicles 0.0154
Kidney	0.0000		Lung 0.0000
Placenta	0.0000		Nerves 0.0000
Prostate	0.0000		Prostate 0.0000
Sensory organs	0.0000		Sensory Organs 0.0000
			Uterus_n

Electronic Northern for SEQ. ID NO.: 4

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0000	undef	0.0000
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0115	0.0000	undef	0.0000
Brain	0.0030	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0021	4.0945	0.2442
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 5

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0256	1.2204	0.8194
Breast	0.0371	0.0282	1.3157	0.7601
Small intestine	0.0368	0.0662	0.5561	1.7982
Ovary	0.0240	0.0494	0.4847	2.0630
Endocrine tissue	0.0324	0.0476	0.6792	1.4722
Gastrointestinal	0.0345	0.0694	0.4970	2.0121
Brain	0.0333	0.0308	1.0799	0.9260
Hematopoietic	0.0388	0.1136	0.3411	2.9315
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0285	0.0065	4.4118	0.2267
Heart	0.0413	0.0137	3.0068	0.3326
Testicles	0.0288	0.0234	1.2299	0.8130
Lung	0.0249	0.0286	0.8709	1.1482
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0171	0.0120	1.4278	0.7004
Kidney	0.0217	0.0479	0.4532	2.2067
Pancreas	0.0132	0.0552	0.2393	4.1785
Penis	0.0479	0.0000	undef	0.0000
Prostate	0.0196	0.0192	1.0236	0.9769
Uterus-endometrium	0.0473	0.0528	0.8962	1.1158
Uterus-myometrium	0.0457	0.0611	0.7482	1.3366
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0448			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0178			
Sensory organs	0.0353			
White blood cells	0.0434			
Cervix	0.0532			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.1809	Breast	0.0204
Gastrointestinal	0.0361	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0101
Hematopoietic	0.0433	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0128
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0640	Hematopoietic	0.0000
Lung	0.0361	Skin-muscle	0.0356
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0371	Lung	0.0246
Placenta	0.0121	Nerves	0.0050
Prostate	0.0000	Prostate	0.0410
Sensory organs	0.0377	Sensory Organs	0.0000
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 6

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0077	0.5085	1.9666
Breast	0.0179	0.0056	3.1758	0.3149
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0153	0.0050	3.0566	0.3272
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0120	0.0379	0.3176	3.1487
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0093	0.0061	1.5241	0.6561
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0000	0.0000	undef	undef
Prostate	0.0087	0.0021	4.0945	0.2442
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0087			
Cervix	0.0000			

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0061	Nerves	0.0020
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0291

Electronic Northern for SEQ. ID NO.: 7

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 8

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0026	4.5763	0.2185
Breast	0.0090	0.0207	0.4331	2.3091
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0180	0.0963	0.1867	5.3565
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0881	0.0694	1.2701	0.7873
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0453	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0125	0.0123	1.0161	0.9842
Stomach-esophagus	0.0387	0.0077	5.0421	0.1983
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0087	0.0511	0.1706	5.8615
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0288			
Prostate hyperplasia	0.0416			
Seminal vesicle	0.1157			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0250	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0253
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0246
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 9

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0273	0.0153	1.7797	0.5619
Breast	0.0077	0.0169	0.4537	2.2042
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0156	0.3838	2.6058
Endocrine tissue	0.0255	0.0376	0.6792	1.4722
Gastrointestinal	0.0211	0.0046	4.5559	0.2195
Brain	0.0111	0.0246	0.4500	2.2223
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0143	0.0129	1.1029	0.9067
Heart	0.0223	0.0137	1.6190	0.6176
Testicles	0.0058	0.0351	0.1640	6.0979
Lung	0.0187	0.0225	0.8313	1.2029
Stomach-esophagus	0.0290	0.0153	1.8908	0.5289
Muscle-skeleton	0.0257	0.0180	1.4278	0.7004
Kidney	0.0081	0.0205	0.3965	2.5219
Pancreas	0.0050	0.0331	0.1496	6.6857
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0305	0.0170	1.7913	0.5582
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.0204	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0268			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0121			
Cervix	0.0213			

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000
Gastrointestinal	0.0139
Brain	0.0063
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0108
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0182
Prostate	0.0499
Sensory organs	0.0000

Breast	0.0204
Ovary_n	0.0000
Ovary_t	0.0304
Endocrine tissue	0.0245
Fetal	0.0047
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0000
Nerves	0.0110
Prostate	0.0068
Sensory Organs	0.0077
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0064	0.0094	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0060	0.0052	1.1513	0.8686
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0007	0.0041	0.1800	5.5559
Hematopoietic	0.0027	0.0758	0.0353	28.3379
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0137	0.3965	2.5219
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0109	0.0043	2.5591	0.3908
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0052			
Cervix	0.0106			

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0080
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 11

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0026	0.0056	0.4537	2.2042
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0090	0.0104	0.8634	1.1582
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0022	0.0031	0.7200	1.3890
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0044	0.0085	0.5118	1.9538
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0304
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0029
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0228
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0154
Kidney	Lung 0.0082
Placenta	Nerves 0.0050
Prostate	Prostate 0.0137
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0077	2.0339	0.4917
Breast	0.0090	0.0056	1.5879	0.6298
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0034	0.0125	0.2717	3.6805
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0052	0.0092	0.5600	1.7858
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0043			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0000
Hematopoietic	0.0118	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0121	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 13

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0051	0.0113	0.4537	2.2042
Small intestine	0.0215	0.0000	undef	0.0000
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0022	0.0041	0.5400	1.8520
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0388	0.1225	8.1599
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0123	0.4234	2.3620
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0163	0.0137	1.1896	0.8406
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0087	0.0000	undef	0.0000
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0068	2.2445	0.4453
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0043			
White blood cells	0.0213			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0072	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0061	Nerves	0.0090
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 14

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0090	0.0026	3.4538	0.2895
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0044	0.0031	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0062	0.0041	1.5241	0.6561
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0000			

FETUS
% frequency

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0204
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0000
Nerves	0.0020
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 15

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef 0.0000	
Breast	0.0038	0.0038	1.0208 0.9796	
Small intestine	0.0000	0.0000	undef undef	
Ovary	0.0000	0.0000	undef undef	
Endocrine tissue	0.0017	0.0025	0.6792 1.4722	
Gastrointestinal	0.0000	0.0000	undef undef	
Brain	0.0044	0.0113	0.3927 2.5464	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0048	0.0000	undef 0.0000	
Heart	0.0021	0.0137	0.1542 6.4853	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0010	0.0020	0.5080 1.9684	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0000	0.0120	0.0000 undef	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0000	0.0166	0.0000 undef	
Penis	0.0000	0.0000	undef undef	
Prostate	0.0000	0.0128	0.0000 undef	
Uterus-endometrium	0.0068	0.0000	undef 0.0000	
Uterus-myometrium	0.0000	0.0068	0.0000 undef	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0060
Placenta	0.0000	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef undef	
Small intestine	0.0026	0.0038	0.6805 1.4694	
Ovary	0.0031	0.0165	0.1854 5.3946	
Endocrine tissue	0.0000	0.0104	0.0000 undef	
Gastrointestinal	0.0000	0.0000	undef undef	
Brain	0.0038	0.0046	0.8283 1.2072	
Hematopoietic	0.0059	0.0041	1.4399 0.6945	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0037	0.0000	undef 0.0000	
Heart	0.0048	0.0000	undef 0.0000	
Testicles	0.0011	0.0000	undef 0.0000	
Lung	0.0058	0.0000	undef 0.0000	
Stomach-esophagus	0.0021	0.0000	undef 0.0000	
Muscle-skeleton	0.0000	0.0077	0.0000 undef	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0109	0.0068	1.5861 0.6305	
Penis	0.0017	0.0221	0.0748 13.3713	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0022	0.0000	undef 0.0000	
Uterus-myometrium	0.0000	0.0528	0.0000 undef	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0000	0.0000	undef undef	
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0058
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0070
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 18

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0117	0.0077	1.5254	0.6555
Small intestine	0.0026	0.0038	0.6805	1.4694
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0136	0.0050	2.7170	0.3681
Brain	0.0038	0.0000	undef	0.0000
Hematopoietic	0.0030	0.0051	0.5760	1.7362
Skin	0.0053	0.0379	0.1412	7.0845
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0194	0.0000	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0031	0.0041	0.7621	1.3122
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0060	0.0000	undef
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0000	0.0166	0.0000	undef
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0109	0.0043	2.5591	0.3908
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0152	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0954	0.0000	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0069			
	0.0000			

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0203
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0035
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0072	Testicles	0.0162
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 19

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0150	0.0052	2.8781	0.3474
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0037	0.0041	0.8999	1.1112
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0031	0.0061	0.5080	1.9684
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0017			
Cervix	0.0000			

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0036
Kidney	0.0000
Placenta	0.0000
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0051
Fetal	0.0000
Gastrointestinal	0.0029
Hematopoietic	0.0122
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0090
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 20

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0007	0.0010	0.7200	1.3890
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0129	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0062	0.0020	3.0482	0.3281
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0000	0.0068	0.0000	undef
Penis	0.0000	0.0221	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0061			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 21

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0051	3.0509	0.3278
Breast	0.0077	0.0056	1.3611	0.7347
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0000	0.0051	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0113	0.0000	undef	0.0000
Lung	0.0000	0.0041	0.0000	undef
Stomach-esophagus	0.0193	0.0230	0.8404	1.1900
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0145
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0476
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0010
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 22

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0037	0.0031	1.1999	0.8334
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0061	0.5080	1.9684
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0208			
Cervix	0.0000			

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0101
Fetal	0.0012
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0077
Lung	0.0000
Nerves	0.0040
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 23

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0020
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0232
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 24

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0102	0.0056	1.8147	0.5510
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0031	0.7200	1.3890
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0194	0.4902	2.0400
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0020	1.5241	0.6561
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0106			

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 25

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0094	0.2722	3.5736
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0017	0.0050	0.3396	2.9444
Gastrointestinal	0.0115	0.0231	0.4970	2.0121
Brain	0.0037	0.0021	1.7999	0.5556
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0275	0.0771	12.9706
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0020	3.5562	0.2812
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0218	0.0341	0.6398	1.5631
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0082
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 26

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 27

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0128	0.0150	0.8507	1.1756
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0359	0.0182	1.9736	0.5067
Endocrine tissue	0.0273	0.0226	1.2076	0.8281
Gastrointestinal	0.0153	0.0185	0.8283	1.2072
Brain	0.0133	0.0144	0.9257	1.0803
Hematopoietic	0.0201	0.0379	0.5293	1.8892
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0048	0.0259	0.1838	5.4400
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0166	0.0123	1.3548	0.7381
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0217	0.0137	1.5861	0.6305
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0153	0.0106	1.4331	0.6978
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0408	0.3741	2.6732
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0087			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0188	Ovary_t	0.0101
Hematopoietic	0.0079	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0186
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0145	Skin-muscle	0.0486
Suprarenal gland	0.0000	Testicles	0.0385
Kidney	0.0247	Lung	0.0328
Placenta	0.0182	Nerves	0.0151
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0333

Electronic Northern for SEQ. ID NO.: 28

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0078	0.0153	0.5085	1.9666
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0210	0.0000	undef	0.0000
Endocrine tissue	0.0068	0.0025	2.7170	0.3681
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0030	0.0051	0.5760	1.7362
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0000	0.0000	undef	undef
Lung	0.0125	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0033	0.0387	0.0855	11.6999
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0063	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0291

Electronic Northern for SEQ. ID NO.: 29

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0020	1.5241	0.6561
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0070
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 30

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0128	0.6102	1.6389
Small intestine	0.0102	0.0244	0.4188	2.3879
Ovary	0.0153	0.0165	0.9268	1.0789
Endocrine tissue	0.0030	0.0026	1.1513	0.8686
Gastrointestinal	0.0017	0.0025	0.6792	1.4722
Brain	0.0115	0.0231	0.4970	2.0121
Hematopoietic	0.0081	0.0175	0.4659	2.1466
Skin	0.0067	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0190	0.0647	0.2941	3.4000
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0115	0.0000	undef	0.0000
Stomach-esophagus	0.0052	0.0143	0.3629	2.7557
Muscle-skeleton	0.0000	0.0537	0.0000	undef
Kidney	0.0120	0.0060	1.9989	0.5003
Pancreas	0.0217	0.0548	0.3965	2.5219
Penis	0.0000	0.0221	0.0000	undef
Prostate	0.0060	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0068	0.0000	undef	0.0000
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0052			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0076
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 31

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0052	0.0062	0.8400	1.1905
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0106	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0954	0.0000	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0247	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 32

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0037	0.0154	0.2400	4.1669
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0137	0.4626	2.1618
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0031	0.0123	0.2540	3.9367
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0387	0.0427	23.3998
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0061			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 33

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0030	0.0031	0.9599	1.0417
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 34

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0013	0.0000	undef	0.0000	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0020	0.0000	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0060	0.0000	undef	
Kidney	0.0000	0.0068	0.0000	undef	
Pancreas	0.0000	0.0166	0.0000	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix	0.0000				

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 35

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 36

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0013	0.0000	undef	0.0000	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0007	0.0000	undef	0.0000	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0221	0.0000	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 37

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0120	0.0026	4.6050	0.2172
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0103	0.0062	1.6799	0.5953
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0043			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0079	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0246
Placenta	0.0121	Nerves	0.0090
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 38

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0038	0.0000	undef	0.0000	
Small intestine	0.0061	0.0000	undef	0.0000	
Ovary	0.0000	0.0026	0.0000	undef	
Endocrine tissue	0.0102	0.0025	4.0755	0.2454	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0030	0.0041	0.7200	1.3890	
Hematopoietic	0.0053	0.0000	undef	0.0000	
Skin	0.0037	0.0000	undef	0.0000	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0021	0.0275	0.0771	12.9706	
Testicles	0.0058	0.0117	0.4920	2.0326	
Lung	0.0042	0.0000	undef	0.0000	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0017	0.0120	0.1428	7.0040	
Kidney	0.0054	0.0068	0.7930	1.2610	
Pancreas	0.0000	0.0166	0.0000	undef	
Penis	0.0030	0.0000	undef	0.0000	
Prostate	0.0022	0.0021	1.0236	0.9769	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0030				
Prostate hyperplasia	0.0178				
Seminal vesicle	0.0000				
Sensory organs	0.0009				
White blood cells	0.0000				
Cervix					

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0254
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0082
Nerves	0.0050
Prostate	0.0205
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 39

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0059	0.0010	5.7597	0.1736
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0043	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 40

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0041	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0043			
White blood cells	0.0106			
Cervix				

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0285
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 41

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0115	0.0075	1.5312	0.6531
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0210	0.0026	3.0588	0.1241
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0067	0.0051	1.2959	0.7716
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0218	0.0192	1.1374	0.8792
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0069			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0612
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 42

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0102	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0111	0.0031	3.5998	0.2778
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0533	0.0562	17.8070
Prostate	0.0109	0.0149	0.7312	1.3677
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0061	Nerves	0.0274
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 43

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0051	1.5254	0.6555
Breast	0.0026	0.0113	0.2268	4.4083
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0136	0.0075	1.8113	0.5521
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0059	0.0092	0.6400	1.5626
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0135	0.0061	2.2015	0.4542
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0033	0.0221	0.1496	6.6857
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0131	0.0128	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0178			
Sensory organs	0.0235			
White blood cells	0.0087			
Cervix	0.0106			

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0101
Hematopoietic	0.0118	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0002
Placenta	0.0121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 44

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0026	9.1527	0.1093
Breast	0.0077	0.0094	0.8166	1.2245
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0000	undef	0.0000
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0057	0.0139	0.4142	2.4145
Brain	0.0015	0.0021	0.7200	1.3890
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0081	0.0137	0.5948	1.6813
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0150	0.0800	0.1872	5.3421
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0078			
Cervix	0.0213			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0056	Ovary_n	0.0408
Brain	0.0000	Ovary_t	0.1595
Hematopoietic	0.0000	Endocrine tissue	0.0101
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0029
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0130
Kidney	0.0000	Lung	0.0154
Placenta	0.0000	Nerves	0.0082
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 45

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0102	0.0000	undef
Breast	0.0051	0.0056	0.9074	1.1021
Small intestine	0.0092	0.0331	0.2781	3.5964
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0052	0.0082	0.6300	1.5874
Hematopoietic	0.0107	0.0379	0.2823	3.5422
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0412	0.0514	19.4559
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0083	0.0020	4.0643	0.2460
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0000	0.0000	undef	undef
Prostate	0.0153	0.0085	1.7913	0.5582
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0069			
Cervix	0.0106			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0340
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0456
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0231
Kidney	0.0062	Lung	0.0410
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 46

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0041	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000		undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 47

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0068	0.0025	2.7170	0.3681
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0044	0.0062	0.7200	1.3890
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0051	0.0060	0.8567	1.1673
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0000			

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0188
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0108
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0245
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0097
Testicles	0.0077
Lung	0.0082
Nerves	0.0131
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 48

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 49

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0130	0.2303	4.3431
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0052	0.0062	0.8400	1.1905
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0020	1.5241	0.6561
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0121	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 50

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 51

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0030	0.0021	1.4399	0.6945
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 52

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0259	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency	% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 53

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0153	0.5085	1.9666
Breast	0.0051	0.0132	0.3889	2.5715
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0030	0.0041	0.7200	1.3890
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0138	0.0000	undef	0.0000
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0276	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0085	0.5118	1.9538
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0156			
Cervix	0.0213			

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0072
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0246
Nerves	0.0050
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 54

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0390	0.0230	1.6949	0.5900
Breast	0.0064	0.0056	1.1342	0.8817
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0270	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0096	0.0046	2.0708	0.4829
Brain	0.0007	0.0041	0.1800	5.5559
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0275	0.0385	25.9412
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0034	0.0120	0.2856	3.5020
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0109	0.0043	2.5591	0.3908
Uterus-endometrium	0.0608	0.0000	undef	0.0000
Uterus-myometrium	0.0610	0.0408	1.4964	0.6683
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 55

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0051	0.0075	0.6805	1.4694
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0150	0.0052	2.8781	0.3474
Endocrine tissue	0.0034	0.0201	0.1698	5.8889
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0096	0.0051	1.8719	0.5342
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0000	0.0275	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0034	0.0120	0.2856	3.5020
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0087			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 56

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0064	0.0000	undef	0.0000
Small intestine	0.0583	0.0662	0.8805	1.1357
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0498	0.0139	3.5895	0.2786
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0323	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0027	0.0000	undef	undef
Kidney	0.0017	0.0331	0.0499	20.0570
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0096			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0082
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 57

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0077	0.0019	4.0832	0.2449
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0037	0.0051	0.7200	1.3890
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0061	0.3387	2.9526
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0022	0.0106	0.2047	4.8846
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0043			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0340
Gastrointestinal 0.0000	Ovary_n 0.0000
Brain 0.0000	Ovary_t 0.0101
Hematopoietic 0.0250	Endocrine tissue 0.0000
Skin 0.0000	Fetal 0.0023
Hepatic 0.0000	Gastrointestinal 0.0000
Heart-blood vessels 0.0000	Hematopoietic 0.0000
Lung 0.0000	Skin-muscle 0.0000
Suprarenal gland 0.0000	Testicles 0.0000
Kidney 0.0062	Lung 0.0082
Placenta 0.0000	Nerves 0.0110
Prostate 0.0000	Prostate 0.0137
Sensory organs 0.0000	Sensory Organs 0.0000
	Uterus_n 0.0000

Electronic Northern for SEQ. ID NO.: 58

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0068	0.0025	2.7170	0.3681
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0082	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0954	0.1067	9.3678
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0353			
White blood cells	0.0000			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0058
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0062	Lung	0.0000
Placenta	0.0061	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 59

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0051	0.7627	1.3111
Small intestine	0.0038	0.0000	undef	0.0000
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0120	0.0052	2.3025	0.4343
Gastrointestinal	0.0034	0.0000	undef	0.0000
Brain	0.0038	0.0093	0.4142	2.4145
Hematopoietic	0.0044	0.0000	undef	0.0000
Skin	0.0013	0.0379	0.0353	28.3379
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0022	0.0064	0.3412	2.9308
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0087			
Cervix	0.0000			

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 60

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0179	0.2179	4.5888
Breast	0.0102	0.0056	1.8147	0.5510
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0085	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0037	0.0164	0.2250	4.4447
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0042	0.0082	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0180	0.0952	10.5060
Kidney	0.0109	0.0205	0.5287	1.8915
Pancreas	0.0017	0.0442	0.0374	26.7427
Penis	0.0000	0.0000	undef	undef
Prostate	0.0131	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0253
Hematopoietic	0.0079	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0227
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0309	Lung	0.0164
Placenta	0.0000	Nerves	0.0070
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 61

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0077	0.5085	1.9666
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0052	1.1513	0.8686
Endocrine tissue	0.0102	0.0150	0.6792	1.4722
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0096	0.0092	1.0399	0.9616
Hematopoietic	0.0107	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0137	0.3855	2.5941
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0021	0.0082	0.2540	3.9367
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0087	0.0064	1.3648	0.7327
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 62

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0331	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 63

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0051	3.0509	0.3278
Breast	0.0128	0.0075	1.7013	0.5878
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0134	0.0000	undef	0.0000
Brain	0.0059	0.0031	1.9199	0.5209
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0286	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0131	0.0043	3.0709	0.3256
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.0068	6.7336	0.1485
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0534			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0182	Nerves	0.0010
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0093

Electronic Northern for SEQ. ID NO.: 64

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0034	0.0125	0.2717	3.6805
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0051	0.7200	1.3890
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0068	4.4891	0.2226
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0087			
White blood cells	0.0106			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0036	Skin-muscle	0.0972
Suprarenal gland	0.0254	Testicles	0.0309
Kidney	0.0000	Lung	0.0410
Placenta	0.0061	Nerves	0.0131
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 65

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000		
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0052			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 66

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0017	0.0050	0.3396	2.9444
Gastrointestinal	0.0153	0.0000	undef	0.0000
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0043	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 67

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0030	0.0031	0.9599	1.0417
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0020	1.5241	0.6561
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0254	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0232
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 68

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0051	0.0060	0.8567	1.1673
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0043			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0242	Nerves	0.0020
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 69

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0013	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 70

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0041	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 71

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0000	undef	0.0000
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0017	0.0100	0.1698	5.8889
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0022	0.0103	0.2160	4.6299
Hematopoietic	0.0027	0.0758	0.0353	28.3379
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0125	0.0061	2.0321	0.4921
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0137	0.0000	undef
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0095			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0810
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0274
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 72

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0030	0.0156	0.1919	5.2117
Endocrine tissue	0.0068	0.0125	0.5434	1.8403
Gastrointestinal	0.0115	0.0000	undef	0.0000
Brain	0.0059	0.0113	0.5236	1.9098
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0052	0.0061	0.8467	1.1810
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0000	0.0000	undef	undef
Prostate	0.0131	0.0064	2.0473	0.4885
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 73

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0102	0.0000	undef
Breast	0.0013	0.0075	0.1701	5.8778
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0068	0.0025	2.7170	0.3681
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0059	0.0031	1.9199	0.5209
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0074	0.0137	0.5397	1.8529
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0120	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0022	0.0085	0.2559	3.9077
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0090
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 74

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0051	4.5763	0.2185
Breast	0.0115	0.0113	1.0208	0.9796
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0210	0.0078	2.6863	0.3723
Endocrine tissue	0.0068	0.0100	0.6792	1.4722
Gastrointestinal	0.0134	0.0000	undef	0.0000
Brain	0.0089	0.0123	0.7200	1.3890
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0062	0.0082	0.7621	1.3122
Stomach-esophagus	0.0097	0.0307	0.3151	3.1733
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0271	0.0205	1.3217	0.7566
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0509	0.0000	undef	0.0000
Prostate	0.0087	0.0128	0.6824	1.4654
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0068	4.4891	0.2228
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0156			
Cervix	0.0106			

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0162
Testicles	0.0000
Lung	0.0082
Nerves	0.0080
Prostate	0.0205
Sensory Organs	0.0000
Uterus_n	0.0708

Electronic Northern for SEQ. ID NO.: 75

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0031	0.7200	1.3890
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0059	0.0000	0.0000
Prostate hyperplasia	0.0000	0.0000	0.0118	0.0000
Seminal vesicle	0.0118	0.0000	0.0000	0.0000
Sensory organs	0.0000	0.0106	0.0000	0.0000
White blood cells	0.0106			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 76

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0120	0.0026	4.6050	0.2172
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0051	0.1908	0.0267	37.4714
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0249	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0063
Suprarenal gland	0.0000	Testicles	0.0231
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 77

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0281	0.0226	1.2476	0.8015
Small intestine	0.0307	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0085	0.0000	undef	0.0000
Gastrointestinal	0.0115	0.0278	0.4142	2.4145
Brain	0.0037	0.0072	0.5143	1.9446
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0061	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0171	0.0180	0.9518	1.0506
Kidney	0.0190	0.0068	2.7756	0.3603
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0139	Breast	0.0476
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0157
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0181	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0303	Nerves	0.0050
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 78

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

		STANDARDIZED/SUBTRACTED LIBRARIES	
FETUS		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 79

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 80

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0429	0.0165	2.5952	0.3853
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0556	0.0185	3.0027	0.3330
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 81

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0234	0.0000	undef
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0214	0.0092	2.3199	0.4311
Hematopoietic	0.0107	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0085	0.0412	0.2056	4.8640
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0082	0.7621	1.3122
Stomach-esophagus	0.0290	0.0383	0.7563	1.3222
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0017	0.0276	0.0598	16.7142
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0353			
White blood cells	0.0095			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0250	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0134
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0518
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0062	Lung	0.0082
Placenta	0.0182	Nerves	0.0141
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 82

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 83

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0077	0.5085	1.9666
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0067	0.0051	1.2959	0.7716
Hematopoietic	0.0107	0.0379	0.2823	3.5422
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0000	0.0137	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0082	0.8891	1.1248
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0121			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0328
Placenta	0.0061	Nerves	0.0070
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 84

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0026	0.0056	0.4537	2.2042
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0089	0.0092	0.9599	1.0417
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0137	0.3855	2.5941
Testicles	0.0000	0.0000	undef	undef
Lung	0.0062	0.0020	3.0482	0.3281
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0022	0.0064	0.3412	2.9308
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0499	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 85

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0153	0.0132	1.1666	0.8572
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0120	0.0208	0.5756	1.7372
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0067	0.0123	0.5400	1.8520
Hematopoietic	0.0134	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0093	0.0102	0.9145	1.0935
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0086	0.0180	0.4759	2.1012
Kidney	0.0027	0.0411	0.0661	15.1317
Pancreas	0.0000	0.0331	0.0000	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0065	0.0149	0.4387	2.2795
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0052			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0139	Breast	0.0068
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0140
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0181	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0121	Nerves	0.0050
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 86

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0064	0.0000	undef	0.0000
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0136	0.0025	5.4340	0.1840
Gastrointestinal	0.0038	0.0046	0.9283	1.2072
Brain	0.0022	0.0082	0.2700	3.7039
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0230	0.0000	undef	0.0000
Lung	0.0042	0.0061	0.6774	1.4763
Stomach-esophagus	0.0097	0.0230	0.4202	2.3799
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0205	0.0000	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0106	0.2047	4.8846
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0353			
White blood cells	0.0035			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 87

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0166	0.0019	8.8469	0.1130
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0115	0.0231	0.4970	2.0121
Brain	0.0118	0.0092	1.2799	0.7813
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0042	0.0061	0.6774	1.4763
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0137	0.0180	0.7615	1.3133
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0109	0.0128	0.8530	1.1723
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0087			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0371	Lung	0.0000
Placenta	0.0061	Nerves	0.0020
Prostate	0.0249	Prostate	0.0137
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 88

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0064	0.0113	0.5671	1.7633
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0052	1.1513	0.8686
Endocrine tissue	0.0136	0.0150	0.9057	1.1042
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0170	0.0113	1.5054	0.6643
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0083	0.0143	0.5806	1.7223
Stomach-esophagus	0.0290	0.0153	1.8908	0.5289
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0033	0.0331	0.0997	10.0285
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0069			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0278	Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0175
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0213	Hematopoietic	0.0114
Lung	0.0181	Skin-muscle	0.0227
Suprarenal gland	0.0254	Testicles	0.0309
Kidney	0.0124	Lung	0.0082
Placenta	0.0182	Nerves	0.0120
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0387
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 90

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0117	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency	% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 91

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0429	0.0767	0.5593	1.7879
Breast	0.0652	0.0320	2.0416	0.4898
Small intestine	0.0061	0.0331	0.1854	5.3946
Ovary	0.0060	0.0000	undef	0.0000
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0153	0.0370	0.4142	2.4145
Brain	0.0126	0.1294	0.0971	10.2947
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0073	0.0123	0.5927	1.6872
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0120	0.0360	0.3331	3.0017
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0033	0.0607	0.0544	18.3856
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0085	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0278	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0272
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Endocrine tissue	0.1224
Hepatic	0.0000	Fetal	0.0093
Heart-blood vessels	0.0213	Gastrointestinal	0.0000
Lung	0.0000	Hematopoietic	0.0000
Suprarenal gland	0.0000	Skin-muscle	0.0000
Kidney	0.0062	Testicles	0.0000
Placenta	0.0000	Lung	0.0000
Prostate	0.0000	Nerves	0.0131
Sensory organs	0.0000	Prostate	0.0137
		Sensory Organs	0.0155
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 92

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0102	0.0132	0.7777	1.2858
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0060	0.0052	1.1313	0.3686
Endocrine tissue	0.0170	0.0100	1.6981	0.5889
Gastrointestinal	0.0115	0.0000	undef	0.0000
Brain	0.0059	0.0041	1.4399	0.6945
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0476	0.1359	0.3501	2.8560
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0062	0.0041	1.5241	0.6561
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0051	0.0060	0.8567	1.1673
Kidney	0.0136	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0479	0.0490	0.9791	1.0213
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0146
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0124	Lung	0.0164
Placenta	0.0061	Nerves	0.0060
Prostate	0.0249	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 93

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0013	0.0000	undef	0.0000
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0061			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0544
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0520	Gastrointestinal	0.0192
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 94

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0090	0.0150	0.5955	1.6794
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0030	0.0078	0.3838	0.6058
Endocrine tissue	0.0136	0.0025	5.4340	0.1840
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0163	0.0082	1.9799	0.5051
Hematopoietic	0.0094	0.0379	0.2470	4.0483
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0139	0.0137	1.1565	0.8647
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0135	0.0102	1.3209	0.7571
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0051	0.0060	0.8567	1.1673
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0033	0.0442	0.0748	13.3713
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0087	0.0021	4.0945	0.2442
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0075	0.0136	0.5611	1.7921
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0356			
Sensory organs	0.0000			
White blood cells	0.0095			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0101
Hematopoietic	0.0188	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0145	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0410
Placenta	0.0182	Nerves	0.0161
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 95

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0064	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0124	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 96

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0115	0.0038	3.0624	0.3263
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0120	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0077	0.0046	1.6567	0.6036
Brain	0.0074	0.0133	0.5538	1.8057
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0257	0.2542	0.1011	9.8931
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0082	0.8891	1.1248
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0306	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0121			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.7538	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0507	Testicles	0.0000
Kidney	0.0000	Lung	0.3154
Placenta	0.0121	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 98

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef undef	
Breast	0.0051	0.0038	1.3611 0.7347	
Small intestine	0.1410	0.0165	8.5270 0.1173	
Ovary	0.0060	0.0052	1.1513 0.8686	
Endocrine tissue	0.0000	0.0025	0.0000 undef	
Gastrointestinal	0.1820	0.0093	19.6731	0.0508
Brain	0.0000	0.0000	undef undef	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0073	0.0000	undef 0.0000	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0145	0.0041	3.5562 0.2812	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0000	0.0205	0.0000 undef	
Pancreas	0.0000	0.0718	0.0000 undef	
Penis	0.0000	0.0000	undef undef	
Prostate	0.0044	0.0000	undef 0.0000	
Uterus-endometrium	0.0069	0.0000	undef 0.0000	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0340
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 99

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0117	0.0128	0.9153	1.0925
Breast	0.0026	0.0132	0.1944	5.1431
Small intestine	0.0213	0.0000	undef	0.0000
Ovary	0.0120	0.0130	0.9210	1.0858
Endocrine tissue	0.0085	0.0226	0.3774	2.6500
Gastrointestinal	0.0096	0.0093	1.0354	0.9658
Brain	0.0133	0.0113	1.1781	0.8488
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0233	0.0000	undef	0.0000
Testicles	0.0230	0.0117	1.9679	0.5082
Lung	0.0156	0.0184	0.8467	1.1810
Stomach-esophagus	0.0290	0.0077	3.7816	0.2644
Muscle-skeleton	0.0188	0.0240	0.7853	1.2735
Kidney	0.0217	0.0274	0.7930	1.2610
Pancreas	0.0033	0.0442	0.0748	13.3713
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0109	0.0213	0.5118	1.9538
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0235	0.0954	0.2669	3.7471
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0043			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0178	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0097
Suprarenal gland	0.0507	Testicles	0.0000
Kidney	0.0185	Lung	0.0000
Placenta	0.0061	Nerves	0.0040
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 100

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0121	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 101

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0050	0.3396	2.9444
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0022	0.0021	1.0799	0.3260
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0066	2.2445	0.4453
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0033	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 102

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0094	0.1361	7.3472
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0017	0.0100	0.1698	5.8889
Gastrointestinal	0.0134	0.0093	1.4496	0.6898
Brain	0.0044	0.0062	0.7200	1.3890
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0412	0.1285	7.7824
Testicles	0.0056	0.0117	0.4920	2.0326
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0087	0.0085	1.0236	0.9769
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0152	0.0204	0.7482	1.3366
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency	% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0182	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 103

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 104

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0102	1.9068	0.5244
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0119	0.0075	1.5849	0.6309
Gastrointestinal	0.0000	0.0185	0.0000	undef
Brain	0.0185	0.0072	2.5713	0.3889
Hematopoietic	0.0040	0.0379	0.1059	9.4460
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0127	0.0137	0.9252	1.0809
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0180	0.0000	undef
Kidney	0.0027	0.0274	0.0991	10.0878
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0104			
Cervix	0.0106			

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0068
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0194
Suprarenal gland	0.0507	Testicles	0.0231
Kidney	0.0000	Lung	0.0082
Placenta	0.0121	Nerves	0.0161
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0464
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 105

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0056	0.4537	2.2042
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0081	0.0031	2.6399	0.3789
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0847	0.0866	11.5419
Hepatic	0.0049	0.0065	0.7353	1.3600
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0123	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0081	0.0205	0.3965	2.5219
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0106	0.4095	2.4403
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0455
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 106

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0399
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 107

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0031	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0331	0.0499	20.0570
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0213	0.3071	3.2564
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 108

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0187	0.0000	undef	0.0000
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0022	0.0103	0.2160	4.6299
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0102	0.0000	undef
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0163	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0106	0.2047	4.8846
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0063
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0087
Hepatic	0.0032	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 109

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0090	0.0075	1.1909	0.8397
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0044	0.0113	0.3927	2.5464
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0020	4.0643	0.2460
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0109	0.0205	0.5287	1.8915
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0085	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0408
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0020
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 110

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0051	0.0132	0.3889	2.5715
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0060	0.0104	0.5756	1.7372
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0089	0.0133	0.6646	1.5047
Hematopoietic	0.0120	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0138	0.0000	undef	0.0000
Testicles	0.0230	0.0117	1.9679	0.5082
Lung	0.0145	0.0041	3.5562	0.2812
Stomach-esophagus	0.0290	0.0230	1.2605	0.7933
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0240	0.0000	undef	0.0000
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0068	4.4891	0.2228
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0319			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0278	Breast	0.0748
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.0000
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0145	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0309	Lung	0.0082
Placenta	0.0121	Nerves	0.0080
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 111

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0061	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 112

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 113

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0038	0.0093	0.4142	2.4145
Brain	0.0052	0.0051	1.0079	0.9921
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0020	1.5241	0.6561
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0276	0.0598	16.7142
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0064	0.3412	2.9308
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0213			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0083	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 114

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0013	0.0036	0.2268	4.4083
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0090	0.0078	1.1513	0.8686
Endocrine tissue	0.0085	0.0201	0.4245	2.3555
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0244	0.0092	2.6399	0.3788
Hematopoietic	0.0013	0.0379	0.0353	28.3379
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0137	0.3084	3.2426
Testicles	0.0403	0.0000	undef	0.0000
Lung	0.0083	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0087	0.0085	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0064	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0052			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0123	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0488
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0386
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0221
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0750	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 115

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0077	0.0038	2.0416	0.4898
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0120	0.0208	0.5756	1.7372
Endocrine tissue	0.0085	0.0000	undef	0.0000
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0059	0.0113	0.5236	1.9098
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0117	0.0275	0.4240	2.3583
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0104	0.0143	0.7258	1.3779
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0017	0.0120	0.1428	7.0040
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0174	0.0043	4.0945	0.2442
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0178	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0000	Nerves	0.0050
Prostate	0.0249	Prostate	0.0205
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 116

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0051	1.5254	0.6555
Breast	0.0064	0.0038	1.7013	0.5878
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0068	0.0075	0.9057	1.1042
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0030	0.0062	0.4800	2.0835
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0099
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0121	Nerves	0.0070
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 117

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0038	0.0169	0.2268	4.4083
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0022	0.0051	0.4320	2.3149
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0020	2.0321	0.4921
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0120	0.5711	1.7510
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0043	1.5354	0.6513
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	
Gastrointestinal	0.0028	Ovary_n	0.0136
Brain	0.0000	Ovary_t	0.1595
Hematopoietic	0.0000	Endocrine tissue	0.0152
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0058
Heart-blood vessels	0.0107	Hematopoietic	0.0244
Lung	0.0036	Skin-muscle	0.0171
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0328
Placenta	0.0000	Nerves	0.0080
Prostate	0.0249	Prostate	0.0274
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 118

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0068	0.0050	1.3585	0.7361
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0052	0.0031	1.6799	0.5953
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0138	0.0137	1.0023	0.9977
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0123	0.3387	2.9526
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.1908	0.0534	18.7357
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0087
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0061	Nerves	0.0080
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 119

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0017	0.0100	0.1698	5.8889
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0059	0.0021	2.8798	0.3472
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0000	0.0205	0.0000	undef
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0118	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0124	Lung	0.0082
Placenta	0.0121	Nerves	0.0040
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 120

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0051	1.5254	0.6555
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0060	0.0533	0.1123	8.9035
Prostate	0.0065	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0163
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0080
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 123

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0026	4.5763	0.2195
Breast	0.0205	0.0075	2.7221	0.3674
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0210	0.0026	8.0588	0.1241
Endocrine tissue	0.0085	0.0125	0.6792	1.4722
Gastrointestinal	0.0096	0.0046	2.0708	0.4829
Brain	0.0037	0.0021	1.7999	0.5556
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0106	0.0137	0.7710	1.2971
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0082	0.8891	1.1248
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0120	0.0360	0.3331	3.0017
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0276	0.0598	16.7142
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0952
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0118	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0246
Placenta	0.0061	Nerves	0.0010
Prostate	0.0499	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0125

Electronic Northern for SEQ. ID NO.: 124

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0102	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0120	0.0052	2.3025	0.4343
Endocrine tissue	0.0068	0.0100	0.6792	1.4722
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0052	0.0031	1.6799	0.5953
Hematopoietic	0.0040	0.0379	0.1059	9.4460
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0137	0.2313	4.3235
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0062	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0153	0.0085	1.7913	0.5582
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0113			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0309	Lung	0.0000
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 125

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0013	0.0038	0.3403	2.9389
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0026	1.1513	0.8686
Gastrointestinal	0.0034	0.0000	undef	0.0000
Brain	0.0000	0.0045	0.0000	undef
Hematopoietic	0.0030	0.0010	2.8798	0.3472
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0032	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0041	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0027	0.0205	0.1322	7.5658
Penis	0.0000	0.0166	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0106	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 126

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0031	0.0496	0.0618	16.1839
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0085	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0059	0.0113	0.5236	1.9098
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0041	1.7781	0.5624
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0043			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0121	Nerves	0.0100
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 127

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0166	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0304
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0167
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 128

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0022	0.0031	0.7200	1.3890
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0020	2.0321	0.4921
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0276	0.0598	16.7142
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles	0.0000
Lung	0.0082
Nerves	0.0000
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 129

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 130

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0038	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0030	0.0021	1.4399	0.6945
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 131

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 132

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0019	0.0000	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0025	0.0000	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0010	0.0000	undef	
Hematopoietic	0.0013	0.0000	undef	0.0000	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0048	0.0000	undef	0.0000	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0117	0.0000	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0017	0.0000	undef	0.0000	
Kidney	0.0081	0.0000	undef	0.0000	
Pancreas	0.0000	0.0166	0.0000	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 133

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 134

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 135

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 136

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0115	0.0094	1.2250	0.8164
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0090	0.0052	1.7269	0.5791
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0113	0.3273	3.0557
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0148	0.0275	0.5397	1.8529
Testicles	0.0000	0.0000	undef	undef
Lung	0.0135	0.0041	3.3022	0.3028
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0240	0.2142	4.6693
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0269	0.0000	undef	0.0000
Prostate	0.0022	0.0128	0.1706	5.8615
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 137

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 138

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	FETUS	% frequency	
	% frequency		
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 139

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0013	0.0000	undef	0.0000	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0025	0.0000	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0021	0.0000	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0011	0.0000	undef	0.0000	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0020	0.0000	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0166	0.0000	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0009				
White blood cells	0.0000				
Cervix					

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 140

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000		
Prostate hyperplasia	0.0000	0.0000		
Seminal vesicle	0.0000	0.0000		
Sensory organs	0.0000	0.0000		
White blood cells	0.0000	0.0000		
Cervix				

		STANDARDIZED/SUBTRACTED	
FETUS		LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 142

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0030	0.0010	2.8798	0.3472
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 143

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 144

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0013	0.0000	undef	0.0000	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0166	0.0000	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0009				
White blood cells	0.0000				
Cervix					

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 145

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0153	0.5085	1.9666
Breast	0.0090	0.0038	2.3818	0.4198
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0136	0.0301	0.4528	2.2083
Gastrointestinal	0.0115	0.0139	0.8283	1.2072
Brain	0.0214	0.0288	0.7457	1.3411
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0156	0.0123	1.2701	0.7873
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0081	0.0137	0.5948	1.6813
Pancreas	0.0017	0.0331	0.0499	20.0570
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0196	0.0106	1.8425	0.5427
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0340	0.2245	4.4553
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0438	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0162
Suprarenal gland	0.0507	Testicles	0.0000
Kidney	0.0185	Lung	0.0082
Placenta	0.0061	Nerves	0.0060
Prostate	0.0499	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 146

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0090	0.0075	1.1909	0.8397
Small intestine	0.0031	0.0331	0.0927	10.7893
Ovary	0.0060	0.0182	0.3289	3.0402
Endocrine tissue	0.0119	0.0176	0.6792	1.4722
Gastrointestinal	0.0115	0.0046	2.4850	0.4024
Brain	0.0074	0.0041	1.7999	0.5556
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0074	0.0137	0.5397	1.8529
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0020	3.0482	0.3281
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0087	0.0128	0.6824	1.4654
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0078			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0278	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0204
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0072	Skin-muscle	0.0194
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0185	Lung	0.0082
Placenta	0.0182	Nerves	0.0100
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0126	Sensory Organs	0.0155
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 147

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0102	1.5254	0.6555
Breast	0.0153	0.0188	0.8166	1.2245
Small intestine	0.0031	0.0331	0.0927	10.7893
Ovary	0.0090	0.0026	3.4538	0.2895
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0096	0.0093	1.0354	0.9658
Brain	0.0096	0.0164	0.5850	1.7095
Hematopoietic	0.0187	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0117	0.0137	0.8481	1.1791
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0125	0.0102	1.2193	0.8202
Stomach-esophagus	0.0097	0.0460	0.2101	4.7599
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0081	0.0137	0.5948	1.6813
Pancreas	0.0017	0.0331	0.0499	20.0570
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0065	0.0064	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0136	1.6834	0.5940
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0234			
White blood cells	0.0213			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0272
Gastrointestinal	0.0250	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0130
Suprarenal gland	0.0507	Testicles	0.0231
Kidney	0.0062	Lung	0.0000
Placenta	0.0061	Nerves	0.0090
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 148

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0153	0.0000	undef
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0015	0.0082	0.1800	5.5559
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0104	0.0102	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0054	0.0411	0.1322	7.5658
Pancreas	0.0000	0.0221	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 149

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0507	0.0256	1.9831	0.5043
Breast	0.0281	0.0263	1.0694	0.9351
Small intestine	0.0368	0.0000	undef	0.0000
Ovary	0.0300	0.0104	2.8781	0.3474
Endocrine tissue	0.0153	0.0100	1.5283	0.6543
Gastrointestinal	0.0115	0.0278	0.4142	2.4145
Brain	0.0192	0.0359	0.5348	1.8698
Hematopoietic	0.0321	0.0379	0.8469	1.1807
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0350	0.0962	0.3635	2.7513
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0291	0.0245	1.1854	0.8436
Stomach-esophagus	0.0387	0.0690	0.5602	1.7850
Muscle-skeleton	0.0343	0.0600	0.5711	1.7510
Kidney	0.0190	0.0068	2.7756	0.3603
Pancreas	0.0050	0.0994	0.0499	20.0570
Penis	0.0269	0.0800	0.3369	2.9678
Prostate	0.0174	0.0149	1.1699	0.8548
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.0068	6.7336	0.1485
Uterus-general	0.0160	0.0000	undef	0.0000
Breast hyperplasia	0.0208			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0353			
Sensory organs	0.0468			
White blood cells	0.0319			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0278	Breast	0.0476
Gastrointestinal	0.0333	Ovary_n	0.0000
Brain	0.0375	Ovary_t	0.0203
Hematopoietic	0.0236	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0107	Hematopoietic	0.0114
Lung	0.0397	Skin-muscle	0.0259
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0247	Lung	0.0164
Placenta	0.0727	Nerves	0.0120
Prostate	0.0249	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0375

Electronic Northern for SEQ. ID NO.: 151

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0546	0.0281	1.9415	0.5151
Breast	0.0550	0.0263	2.0902	0.4784
Small intestine	0.0368	0.0331	1.1122	0.8991
Ovary	0.0329	0.0338	0.9741	1.0265
Endocrine tissue	0.0085	0.0050	1.6981	0.5889
Gastrointestinal	0.0536	0.0139	3.8656	0.2587
Brain	0.0222	0.0308	0.7200	1.3890
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0808	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0286	0.0275	1.0408	0.9608
Testicles	0.0288	0.0351	0.8200	1.2196
Lung	0.0395	0.0164	2.4132	0.4144
Stomach-esophagus	0.0870	0.0077	11.3448	0.0881
Muscle-skeleton	0.0531	0.0420	1.2646	0.7908
Kidney	0.0244	0.0548	0.4461	2.2417
Pancreas	0.0033	0.0221	0.1496	6.6857
Penis	0.0569	0.0000	undef	0.0000
Prostate	0.0283	0.0255	1.1089	0.9018
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0272	1.1223	0.8911
Uterus-general	0.0764	0.0000	undef	0.0000
Breast hyperplasia	0.0799			
Prostate hyperplasia	0.0327			
Seminal vesicle	0.0445			
Sensory organs	0.0235			
White blood cells	0.0139			
Cervix	0.0958			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0194	Ovary_n	0.3190
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0111
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0107	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0328
Placenta	0.0242	Nerves	0.0030
Prostate	0.0000	Prostate	0.0479
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

Electronic Northern for SEQ. ID NO.: 153

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0690	0.2825	3.5400
Breast	0.0179	0.0320	0.5604	1.7843
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0150	0.0130	1.1513	0.8686
Endocrine tissue	0.0085	0.0100	0.8491	1.1778
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0081	0.0442	0.1842	5.4296
Hematopoietic	0.0187	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0238	0.0194	1.2255	0.8160
Heart	0.0625	0.1649	0.3791	2.6381
Testicles	0.0403	0.0117	3.4438	0.2904
Lung	0.0343	0.0286	1.1975	0.8351
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0668	0.1200	0.5568	1.7959
Kidney	0.0190	0.0342	0.5551	1.8014
Pancreas	0.0050	0.1160	0.0427	23.3998
Penis	0.0329	0.0000	undef	0.0000
Prostate	0.0131	0.0170	0.7677	1.3026
Uterus-endometrium	0.0068	0.0528	0.1280	7.8106
Uterus-myometrium	0.0457	0.0204	2.2445	0.4455
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0356			
Sensory organs	0.0588			
White blood cells	0.0000			
Cervix	0.0319			

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0340
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0118	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0309
Hepatic	0.0520	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0325	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0494	Lung	0.0082
Placenta	0.0909	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 154

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0230	0.6780	1.4750
Breast	0.0256	0.0263	0.9722	1.0286
Small intestine	0.0184	0.0331	0.5561	1.7982
Ovary	0.0150	0.0208	0.7195	1.3898
Endocrine tissue	0.0238	0.0176	1.3585	0.7361
Gastrointestinal	0.0268	0.0185	1.4496	0.6898
Brain	0.0126	0.0205	0.6120	1.6341
Hematopoietic	0.0174	0.0379	0.4587	2.1798
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0288	0.0000	undef	0.0000
Lung	0.0156	0.0123	1.2701	0.7873
Stomach-esophagus	0.0097	0.0307	0.3151	3.1733
Muscle-skeleton	0.0051	0.0180	0.2856	3.5020
Kidney	0.0163	0.0137	1.1896	0.8406
Pancreas	0.0000	0.0497	0.0000	undef
Penis	0.0180	0.0267	0.6739	1.4839
Prostate	0.0196	0.0277	0.7087	1.4111
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0136	2.2445	0.4455
Uterus-general	0.0509	0.0954	0.5337	1.8736
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0267			
Sensory organs	0.0235			
White blood cells	0.0043			
Cervix	0.0319			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0139	Breast	0.0272
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.1772
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0058
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0364	Nerves	0.0020
Prostate	0.0249	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 155

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000 undef	
Breast	0.0038	0.0019	2.0416 0.4898	
Small intestine	0.0061	0.0000	undef 0.0000	
Ovary	0.0030	0.0000	undef 0.0000	
Endocrine tissue	0.0017	0.0075	0.2264 4.4166	
Gastrointestinal	0.0000	0.0000	undef undef	
Brain	0.0015	0.0051	0.2880 3.4724	
Hematopoietic	0.0067	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0032	0.0000	undef 0.0000	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.0097	0.0077	1.2605 0.7933	
Muscle-skeleton	0.0017	0.0000	undef 0.0000	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0000	0.0166	0.0000 undef	
Penis	0.0030	0.0000	undef 0.0000	
Prostate	0.0022	0.0000	undef 0.0000	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0076	0.0000	undef 0.0000	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0000	0.0000	undef undef	
Prostate hyperplasia	0.0030	0.0000	undef 0.0000	
Seminal vesicle	0.0000	0.0000	undef undef	
Sensory organs	0.0043	0.0000	undef 0.0000	
White blood cells	0.0000	0.0000	undef undef	
Cervix	0.0000	0.0000	undef undef	

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0040
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0155
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 156

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0102	1.9068	0.5244
Breast	0.0038	0.0113	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0208	0.2878	3.4745
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0057	0.0139	0.4142	2.4145
Brain	0.0096	0.0051	1.8719	0.5342
Hematopoietic	0.0053	0.0758	0.0706	14.1689
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0127	0.0000	undef	0.0000
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0104	0.0123	0.8467	1.1810
Stomach-esophagus	0.0580	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0180	0.3807	2.6265
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0087	0.0085	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0156			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0253
Hematopoietic	0.0118	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0488
Heart-blood vessels	0.0178	Hematopoietic	0.0171
Lung	0.0036	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0328
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0291

Electronic Northern for SEQ. ID NO.: 157

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0077	0.0132	0.5833	1.7144
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0090	0.0156	0.5756	1.7372
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0103	0.0164	0.6300	1.5874
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0148	0.0137	1.0794	0.9265
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0033	0.0497	0.0665	15.0427
Penis	0.0060	0.0800	0.0749	13.3552
Prostate	0.0065	0.0043	1.5354	0.6513
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0052			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0188	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0030
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for Seq. ID: 597

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0009	0.0042	0.2087	4.7908
Large intestine	0.0000	0.0057	0.0000	undef
Small intestine	0.0027	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0019	0.0018	1.0524	0.9502
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0221	0.0000	undef
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0075	0.0000	undef
White blood cells	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0021	0.0000	undef	0.0000
Penis	0.0013			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 598

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0097	0.0155	0.6262 1.5969
Large intestine	0.0134	0.0114	1.1774 0.8493
Small intestine	0.0082	0.0107	0.7730 1.2937
Ovary	0.0000	0.0048	0.0000 undef
Endocrine tissue	0.0048	0.0053	0.9054 1.1045
Brain	0.0046	0.0040	1.1605 0.8617
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0041	0.0275	0.1477 6.7715
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0068	0.0037	1.8417 0.5430
Stomach-esophagus	0.0145	0.0000	undef 0.0000
Muscle-skeleton	0.0051	0.0037	1.3917 0.7186
Kidney	0.0022	0.0000	undef 0.0000
Pancreas	0.0000	0.0166	0.0000 undef
Prostate	0.0273	0.0300	0.9123 1.0962
T lymphoma	0.0076	0.0224	0.3381 2.9576
Uterus	0.0059	0.0092	0.6426 1.5563
White blood cells	0.0068	0.0000	undef 0.0000
Hematopoietic	0.0067		
Penis	0.0054		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0303
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine t	0.0000
Ovary n	0.0000
Ovary t	0.0354
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles n	0.0042
Testicles t	0.0000
Lungs n	0.0098
Lungs t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary uterus	0.0180
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 599

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0078	0.0164	0.4741 2.1091
Breast	0.0009	0.0000	undef 0.0000
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0237	0.0000	undef 0.0000
Endocrine tissue	0.0064	0.0035	1.8107 0.5523
Brain	0.0029	0.0050	0.5803 1.7234
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0030	0.0137	0.2215 4.5144
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0126	0.0018	6.8408 0.1462
Stomach-esophagus	0.0000	0.0256	0.0000 undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0000	0.0048	0.0000 undef
Pancreas	0.0033	0.0331	0.0997 10.0282
Prostate	0.0038	0.0000	undef 0.0000
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0074	0.0000	undef 0.0000
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0027		
Penis	0.0161		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0245
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0209
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary uterus	0.0225
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 600

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0136	0.7358 1.3590
Bladder	0.0039	0.0117	0.3319 3.0130
Breast	0.0044	0.0014	3.1311 0.3194
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0137	0.0000	undef 0.0000
Ovary	0.0059	0.0024	2.4887 0.4018
Endocrine tissue	0.0032	0.0000	undef 0.0000
Brain	0.0052	0.0140	0.3730 2.6808
Skin	0.0000	0.0000	undef undef
Hepatic	0.0046	0.0000	undef 0.0000
Heart	0.0061	0.0137	0.4430 2.2572
Testicles	0.0120	0.0000	undef 0.0000
Lung	0.0049	0.0111	0.4385 2.2804
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0103	0.0037	2.7833 0.3593
Kidney	0.0067	0.0048	1.3927 0.7180
Pancreas	0.0017	0.0387	0.0427 23.3992
Prostate	0.0019	0.0013	1.4470 0.6911
T lymphoma	0.0051	0.0000	undef 0.0000
Uterus	0.0059	0.0000	undef 0.0000
White blood cells	0.0048	0.0000	undef 0.0000
Hematopoietic	0.0067		
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0188
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0108
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0093
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0070
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 601

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0023	0.0000	undef
Breast	0.0009	0.0000	undef	0.0000
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0027	0.0107	0.2577	3.8812
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0020	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0019	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0037	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Prostate	0.0019	0.0000	undef	0.0000
T lymphoma	0.0051	0.0000	undef	0.0000
Uterus	0.0015	0.0000	undef	0.0000
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0013			
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0039
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0036
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0249
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0051
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 602

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0234	0.0047	4.9788 0.2009
Breast	0.0070	0.0098	0.7157 1.3973
Large intestine	0.0057	0.0085	0.6728 1.4864
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0059	0.0000	undef 0.0000
Endocrine tissue	0.0032	0.0038	0.8479 1.1794
Brain	0.0018	0.0020	0.9068 1.1028
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0046	0.0190	0.2441 4.0960
Heart	0.0081	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0068	0.0018	3.6834 0.2715
Stomach-esophagus	0.0072	0.0064	1.1333 0.8824
Muscle-skeleton	0.0069	0.0000	undef 0.0000
Kidney	0.0067	0.0096	0.6963 1.4362
Pancreas	0.0033	0.0221	0.1496 6.6857
Prostate	0.0094	0.0052	1.8088 0.5529
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0093	0.0000	undef 0.0000
White blood cells	0.0068	0.0000	undef 0.0000
Hematopoietic	0.0000		
Penis	0.0134		
Seminal vesicle	0.0070		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary Uterus	0.0068
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 603

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0141	0.0028	5.0097	0.1996
Large intestine	0.2491	0.0199	12.4946	0.0800
Small intestine	0.1949	0.5326	0.3659	2.7333
Ovary	0.0059	0.0072	0.8296	1.2055
Endocrine tissue	0.0000	0.0035	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0381	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0204	0.0055	3.6835	0.2715
Stomach-esophagus	0.0000	0.0064	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0022	0.0096	0.2321	4.3081
Pancreas	0.0017	0.1105	0.0150	66.8548
Prostate	0.0047	0.0000	undef	0.0000
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0059	0.0000	undef	0.0000
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0000			
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0235			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0610
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0000
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 604

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0136	0.1840 5.4361
Bladder	0.0078	0.0000	undef 0.0000
Breast	0.0079	0.0028	2.8179 0.3549
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0030	0.0048	0.6222 1.6073
Endocrine tissue	0.0032	0.0053	0.6036 1.6568
Brain	0.0058	0.0050	1.1605 0.8617
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0020	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0029	0.0055	0.5262 1.9004
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0022	0.0000	undef 0.0000
Pancreas	0.0017	0.0166	0.0997 10.0282
Prostate	0.0057	0.0078	0.7235 1.3821
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0059	0.0000	undef 0.0000
White blood cells	0.0041	0.0000	undef 0.0000
Hematopoietic	0.0013		
Penis	0.0054		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0250
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0257
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0121
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 605

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0400	0.0000	undef 0.0000
Bladder	0.0078	0.0329	0.2371 4.2182
Breast	0.0141	0.0197	0.7157 1.3973
Large intestine	0.0345	0.0171	2.0184 0.4955
Small intestine	0.0384	0.0320	1.2024 0.8317
Ovary	0.0089	0.0215	0.4148 2.4109
Endocrine tissue	0.0273	0.0319	0.8551 1.1695
Brain	0.0312	0.0299	1.0445 0.9574
Skin	0.0147	0.0000	undef 0.0000
Hepatic	0.0139	0.0317	0.4395 2.2755
Heart	0.0203	0.0275	0.7384 1.3543
Testicles	0.0361	0.0710	0.5089 1.9650
Lung	0.0126	0.0351	0.3600 2.7775
Stomach-esophagus	0.0217	0.0384	0.5668 1.7644
Muscle-skeleton	0.0428	0.0185	2.3194 0.4311
Kidney	0.0179	0.0193	0.9285 1.0770
Pancreas	0.0066	0.0387	0.1709 5.8498
Prostate	0.0160	0.0182	0.8786 1.1382
T lymphoma	0.0278	0.0149	1.8596 0.5377
Uterus	0.0177	0.0046	3.8554 0.2594
White blood cells	0.0192	0.0000	undef 0.0000
Hematopoietic	0.0267		
Penis	0.0161		
Seminal vesicle	0.0141		
Sensory organs	0.0235		

FETUS
% freq.

Development	0.0278
Gastrointestinal	0.0194
Brain	0.0250
Hematopoietic	0.0354
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0640
Lung	0.0289
Adrenal gland	0.0000
Kidney	0.0185
Placenta	0.0364
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.1469
Endocrine tissue	0.0000
Fetal	0.0249
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0281
Kidney t	0.0000
Ovary uterus	0.0833
Prostate n	0.0061
Sensory organs	0.0465
White blood cells	0.0000

Electronic Northern for Seq. ID: 606

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0195	0.0070	2.7658	0.3616
Breast	0.0132	0.0084	1.5655	0.6388
Large intestine	0.0153	0.0000	undef	0.0000
Small intestine	0.0027	0.0000	undef	0.0000
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0000	0.0053	0.0000	undef
Brain	0.0046	0.0040	1.1605	0.8617
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0304	0.0000	undef	0.0000
Testicles	0.0080	0.0000	undef	0.0000
Lung	0.0068	0.0018	3.6835	0.2715
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0037	2.7833	0.3593
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0276	0.0000	undef
Prostate	0.0132	0.0078	1.6882	0.5923
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0222	0.0046	4.8192	0.2075
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0027			
Penis	0.0295			
Seminal vesicle	0.0493			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0000
Sensory organs	0.0155
White blood cells	0.0000

Electronic Northern for Seq. ID: 607

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0014	0.0000	undef
Large intestine	0.0038	0.0057	0.6728	1.4864
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0032	0.0038	0.8479	1.1794
Brain	0.0054	0.0060	0.9068	1.1028
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0127	0.0000	undef
Heart	0.0010	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0039	0.0055	0.7016	1.4253
Stomach-esophagus	0.0000	0.0064	0.0000	undef
Muscle-skeleton	0.0017	0.0037	0.4639	2.1557
Kidney	0.0022	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0286
Prostate	0.0038	0.0013	2.8940	0.3455
T lymphoma	0.0000	0.0075	0.0000	undef
Uterus	0.0015	0.0138	0.1123	8.9083
White blood cells	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0013			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0070
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0310
White blood cells	0.0000

Electronic Northern for Seq. ID: 608

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0150	0.0000	undef 0.0000
Bladder	0.0000	0.0047	0.0000 undef
Breast	0.0018	0.0000	undef 0.0000
Large intestine	0.0019	0.0000	undef 0.0000
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0016	0.0124	0.1293 7.7318
Brain	0.0058	0.0000	undef 0.0000
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0020	0.0000	undef 0.0000
Testicles	0.0040	0.0059	0.6786 1.4737
Lung	0.0019	0.0037	0.5262 1.9004
Stomach-esophagus	0.0145	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0045	0.0048	0.9285 1.0770
Pancreas	0.0017	0.0221	0.0748 13.3710
Prostate	0.0019	0.0000	undef 0.0000
T lymphoma	0.0051	0.0000	undef 0.0000
Uterus	0.0030	0.0000	undef 0.0000
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0053		
Penis	0.0000		
Seminal vesicle	0.0070		
Sensory organs	0.0235		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine t	0.0000
Ovary n	0.1595
Ovary t	0.0000
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles n	0.0000
Testicles t	0.0000
Lungs n	0.0000
Lungs t	0.0000
Nerves	0.0090
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 609

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0078	0.0023	3.3190 0.3013
Breast	0.0035	0.0042	0.8349 1.1977
Large intestine	0.0115	0.0000	undef 0.0000
Small intestine	0.0137	0.0000	undef 0.0000
Ovary	0.0030	0.0143	0.2074 4.8219
Endocrine tissue	0.0064	0.0160	0.4024 2.4852
Brain	0.0041	0.0080	0.5077 1.9696
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0051	0.0000	undef 0.0000
Testicles	0.0080	0.0059	1.3571 0.7369
Lung	0.0049	0.0055	0.8770 1.1402
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0069	0.0037	1.8555 0.5389
Kidney	0.0000	0.0048	0.0000 undef
Pancreas	0.0017	0.0166	0.0997 10.0282
Prostate	0.0104	0.0026	3.9794 0.2513
T lymphoma	0.0051	0.0075	0.6762 1.4788
Uterus	0.0044	0.0046	0.9638 1.0375
White blood cells	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0040		
Penis	0.0000		
Seminal vesicle	0.0070		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 610

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0026	0.0042	0.6262	1.5969
Large intestine	0.0019	0.0028	0.6728	1.4864
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0046	0.0000	undef	0.0000
Heart	0.0010	0.0000	undef	0.0000
Testicles	0.0161	0.0000	undef	0.0000
Lung	0.0000	0.0018	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0022	0.0000	undef	0.0000
Pancreas	0.0017	0.0166	0.0997	10.0286
Prostate	0.0000	0.0013	0.0000	undef
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0015	0.0046	0.3368	2.9694
White blood cells	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0013			
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 611

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0050	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Large intestine	0.0019	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0016	0.0018	0.9054	1.1045
Brain	0.0012	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0010	0.0275	0.0369	27.0862
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0037	0.4639	2.1557
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0166	0.0997	10.0282
Prostate	0.0000	0.0039	0.0000	undef
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0015	0.0000	undef	0.0000
White blood cells	0.0055	0.0000	undef	0.0000
Hematopoietic	0.0067			
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0520
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0612
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0209
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 612

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0075	0.0000	undef	0.0000
Bladder	0.0078	0.0117	0.6638	1.5064
Breast	0.0114	0.0169	0.6784	1.4741
Large intestine	0.0115	0.0085	1.3456	0.7432
Small intestine	0.0110	0.0107	1.0306	0.9703
Ovary	0.0059	0.0072	0.8295	1.2055
Endocrine tissue	0.0144	0.0038	3.8156	0.2621
Brain	0.0193	0.0110	1.7586	0.5686
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0000	0.0190	0.0000	undef
Heart	0.0173	0.0137	1.2552	0.7967
Testicles	0.0080	0.0059	1.3570	0.7369
Lung	0.0165	0.0111	1.4909	0.6707
Stomach-esophagus	0.0000	0.0128	0.0000	undef
Muscle-skeleton	0.0051	0.0037	1.3917	0.7186
Kidney	0.0179	0.0048	3.7136	0.2693
Pancreas	0.0033	0.0442	0.0748	13.3714
Prostate	0.0085	0.0039	2.1705	0.4607
T lymphoma	0.0101	0.0075	1.3525	0.7394
Uterus	0.0093	0.0138	0.6735	1.4847
White blood cells	0.0096	0.0304	0.3156	3.1685
Hematopoietic	0.0094			
Penis	0.0134			
Seminal vesicle	0.0352			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0185
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0244
Hematopoietic	0.0513
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0586
Lungs_t	0.0000
Nerves	0.0161
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0182
Sensory organs	0.0077
White blood cells	0.0000

Electronic Northern for Seq. ID: 613

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0053	0.0000	undef	0.0000
Large intestine	0.0000	0.0028	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0032	0.0000	undef	0.0000
Brain	0.0000	0.0010	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0010	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0029	0.0000	undef	0.0000
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0166	0.0000	undef
Prostate	0.0009	0.0013	0.7235	1.3821
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0015	0.0000	undef	0.0000
White blood cells	0.0021	0.0000	undef	0.0000
Hematopoietic	0.0000			
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 614

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0272	0.1840 5.4361
Bladder	0.0039	0.0000	undef 0.0000
Breast	0.0070	0.0000	undef 0.0000
Large intestine	0.0096	0.0057	1.6820 0.5945
Small intestine	0.0082	0.0107	0.7730 1.2937
Ovary	0.0000	0.0048	0.0000 undef
Endocrine tissue	0.0177	0.0057	3.1090 0.3216
Brain	0.0030	0.0130	0.2325 4.3010
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0232	0.0000	undef 0.0000
Heart	0.0041	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0019	0.0092	0.2105 4.7510
Stomach-esophagus	0.0000	0.0128	0.0000 undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0134	0.0000	undef 0.0000
Pancreas	0.0033	0.0166	0.1994 5.0143
Prostate	0.0094	0.0078	1.2058 0.8293
T lymphoma	0.0126	0.0000	undef 0.0000
Uterus	0.0015	0.0000	undef 0.0000
White blood cells	0.0048	0.0000	undef 0.0000
Hematopoietic	0.0107		
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0151
Gastrointestinal	0.0000
Hematopoietic	0.0257
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0070
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0121
Sensory organs	0.0232
White blood cells	0.0000

Electronic Northern for Seq. ID: 615

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0009	0.0028	0.3131	3.1939
Large intestine	0.0000	0.0057	0.0000	undef
Small intestine	0.0055	0.0000	undef	0.0000
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0018	0.0010	1.8135	0.5514
Skin	0.0073	0.0394	0.1862	5.3703
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0059	0.0000	undef
Lung	0.0039	0.0037	1.0524	0.9502
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0022	0.0000	undef	0.0000
Pancreas	0.0000	0.0221	0.0000	undef
Prostate	0.0019	0.0013	1.4470	0.6911
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0013			
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0181
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 616

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0094	0.0000 undef
Breast	0.0070	0.0098	0.7157 1.3973
Large intestine	0.0057	0.0114	0.5046 1.9818
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0119	0.0024	4.9773 0.2009
Endocrine tissue	0.0112	0.0071	1.5844 0.6312
Brain	0.0075	0.0070	1.0776 0.9280
Skin	0.0037	0.0394	0.0931 10.7394
Hepatic	0.0000	0.0000	undef undef
Heart	0.0041	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0039	0.0037	1.0524 0.9502
Stomach-esophagus	0.0145	0.0064	2.2671 0.4411
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0045	0.0000	undef 0.0000
Pancreas	0.0050	0.0276	0.1795 5.5712
Prostate	0.0094	0.0065	1.4470 0.6911
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0044	0.0000	undef 0.0000
White blood cells	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0053		
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0513
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0040
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 617

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0018	0.0028	0.6262 1.5969
Large intestine	0.0019	0.0028	0.6728 1.4864
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0030	0.0072	0.4148 2.4110
Endocrine tissue	0.0016	0.0019	0.8479 1.1794
Brain	0.0036	0.0020	1.8135 0.5514
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0051	0.0137	0.3692 2.7087
Testicles	0.0000	0.0118	0.0000 undef
Lung	0.0019	0.0055	0.3508 2.8506
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0037	0.9278 1.0778
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0166	0.0000 undef
Prostate	0.0028	0.0000	undef 0.0000
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0000	0.0046	0.0000 undef
White blood cells	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0040		
Penis	0.0054		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

2.2. Fisher Test

In order to decide whether a partial sequence *S* of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to *S*. If the null hypothesis can be rejected with high enough certainty, the gene belonging to *S* is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence *S* is completed in three steps:

1. Determination of all sequences homologous to *S* from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F., and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence *C* from the assembled sequences.

Consensus sequence *C* will generally be longer than initial sequence *S*. Its electronic Northern Blot will accordingly

deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i: iteration index) obtained in each case until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from pancreas tumor tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

Example 4**Mapping of Nucleic Acid Sequences on the Human Genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining Genomic DNA Sequences (BAC Clones)

The genomic BAC clones containing the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well". In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

<u>Seq. ID No.</u>	<u>Identified BACs</u>		
22	266/N/19	393/M/5	504/A/18

Col. 1 - Sequence ID No.

Col. 2 - Expression

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Cytogenetic localization

Col. 6 - Nearest marker

TABLE I

Sequence ID No.	Expression	Function
1	Overexpressed in the pancreas tumor tissue	Unknown
2	Overexpressed in the pancreas tumor tissue	Unknown
3	Overexpressed in the pancreas tumor tissue	Human homolog to M. musculus chromaffin granule ATPase II
4	Overexpressed in the pancreas tumor tissue	Unknown
5	Overexpressed in the pancreas tumor tissue	HMG-1
6	Overexpressed in the pancreas tumor tissue	NY-CO-41
7	Overexpressed in the pancreas tumor tissue	Unknown
8	Overexpressed in the pancreas tumor tissue	Human homolog to M. musculus GOB-4
9	Overexpressed in the pancreas tumor tissue	Human homolog to B. laurus epsilon-COP
10	Overexpressed in the pancreas tumor tissue	Pyrophosphatase

11	Overexpressed in the pancreas tumor tissue	Unknown
12	Overexpressed in the pancreas tumor tissue	Human homolog to X. laevis dependent RNA helicase
13	Overexpressed in the pancreas tumor tissue	Unknown
14	Overexpressed in the pancreas tumor tissue	Unknown
15	Overexpressed in the pancreas tumor tissue	Unknown
16	Overexpressed in the pancreas tumor tissue	Unknown
17	Overexpressed in the pancreas tumor tissue	Unknown
18	Overexpressed in the pancreas tumor tissue	Unknown
19	Overexpressed in the pancreas tumor tissue	Unknown
20	Overexpressed in the pancreas tumor tissue	Unknown
21	Overexpressed in the pancreas tumor tissue	Unknown

22	Overexpressed in the pancreas tumor tissue	Unknown
23	Overexpressed in the pancreas tumor tissue	Unknown
24	Overexpressed in the pancreas tumor tissue	Unknown
25	Overexpressed in the pancreas tumor tissue	Unknown
26	Overexpressed in the pancreas tumor tissue	Unknown
27	Overexpressed in the pancreas tumor tissue	Unknown
28	Overexpressed in the pancreas tumor tissue	Unknown
29	Overexpressed in the pancreas tumor tissue	Unknown
30	Overexpressed in the pancreas tumor tissue	Unknown
31	Overexpressed in the pancreas tumor tissue	Unknown
32	Overexpressed in the pancreas tumor tissue	Unknown

33	Overexpressed in the pancreas tumor tissue	Unknown
34	Overexpressed in the pancreas tumor tissue	Unknown
35	Overexpressed in the pancreas tumor tissue	Unknown
36	Overexpressed in the pancreas tumor tissue	Unknown
37	Overexpressed in the pancreas tumor tissue	Human homolog to M. musculus NIK
38	Overexpressed in the pancreas tumor tissue	Human homolog to molybdoterin biosynthesis MOEB protein
39	Overexpressed in the pancreas tumor tissue	Unknown
40	Overexpressed in the pancreas tumor tissue	Unknown
41	Overexpressed in the pancreas tumor tissue	Unknown
42	Overexpressed in the pancreas tumor tissue	Fas-ligand associated factor 3
43	Overexpressed in the pancreas tumor tissue	Human homolog to M. musculus SH3P7

44	Overexpressed in the pancreas tumor tissue	Human homolog to <i>C. elegans</i> FER-1
45	Overexpressed in the pancreas tumor tissue	Human homolog to <i>C. griseus</i> ars2
46	Overexpressed in the pancreas tumor tissue	Human homolog to a man(9)-alpha- mannosidase-like protein of <i>C.</i> <i>elegans</i>
47	Overexpressed in the pancreas tumor tissue	JM4
48	Overexpressed in the pancreas tumor tissue	Homologous to cyclin C (CCNC)
49	Overexpressed in the pancreas tumor tissue	Homologous to VAMP associated protein of 33kDa
50	Overexpressed in the pancreas tumor tissue	Homologous to prepromultimerin
51	Overexpressed in the pancreas tumor tissue	Unknown
52	Overexpressed in the pancreas tumor tissue	Homologous to fructose-1,6- biphosphatase
53	Overexpressed in the pancreas tumor tissue	Unknown
54	Overexpressed in the pancreas tumor tissue	Hic-5

55	Overexpressed in the pancreas tumor tissue	Unknown
56	Overexpressed in the pancreas tumor tissue	Polymeric immunoglobulin receptor
57	Overexpressed in the pancreas tumor tissue	Human homolog to H. beta 58
58	Overexpressed in the pancreas tumor tissue	Human homolog to R. norvegicus TIP49
59	Overexpressed in the pancreas tumor tissue	Human homolog to R. norvegicus ABP- 7
60	Overexpressed in the pancreas tumor tissue	Agrin
61	Overexpressed in the pancreas tumor tissue	Triose-phosphate isomerase
63	Overexpressed in the pancreas tumor tissue	Human homolog to M. musculus polymerase I-transcript release factor
64	Overexpressed in the pancreas tumor tissue	Human homolog to M. musculus AP19
65	Overexpressed in the pancreas tumor tissue	Homologous to Ras inhibitor
66	Overexpressed in the pancreas tumor tissue	Unknown

67	Overexpressed in the pancreas tumor tissue	Human homolog to <i>S. pombe</i> POP3
68	Overexpressed in the pancreas tumor tissue	Unknown
69	Overexpressed in the pancreas tumor tissue	Unknown
70	Overexpressed in the pancreas tumor tissue	Unknown
71	Overexpressed in the pancreas tumor tissue	Homologous to APRIL
72	Overexpressed in the pancreas tumor tissue	Unknown
73	Overexpressed in the pancreas tumor tissue	Unknown
74	Overexpressed in the pancreas tumor tissue	SH3 domain binding glutamic acid- rich-like protein
75	Overexpressed in the pancreas tumor tissue	Unknown
76	Overexpressed in the pancreas tumor tissue	KE04p
77	Overexpressed in the pancreas tumor tissue	Unknown

78	Overexpressed in the pancreas tumor tissue	Unknown
79	Overexpressed in the pancreas tumor tissue	Unknown
80	Overexpressed in the pancreas tumor tissue	Human homolog to M. musculus cell surface antigen 114/A10
81	Overexpressed in the pancreas tumor tissue	Human homolog to R. norvegicus RNH-1/14-3-3
82	Overexpressed in the pancreas tumor tissue	Unknown
83	Overexpressed in the pancreas tumor tissue	Unknown
84	Overexpressed in the pancreas tumor tissue	Unknown
85	Overexpressed in the pancreas tumor tissue	hD54
86	Overexpressed in the pancreas tumor tissue	Unknown
87	Overexpressed in the pancreas tumor tissue	Human homolog to S. pombe TPR
88	Overexpressed in the pancreas tumor tissue	Human homolog to M. musculus seizure-related mRNA

90	Overexpressed in the pancreas tumor tissue	Human KIP2 gene for Cdk-inhibitor p57KIP2 homolog
91	Overexpressed in the pancreas tumor tissue	sFRP-2
92	Overexpressed in the pancreas tumor tissue	Homologous to lung carbonyl reductase
93	Overexpressed in the pancreas tumor tissue	Human homolog to C. elegans MSR4 like protein
94	Overexpressed in the pancreas tumor tissue	Unknown
95	Overexpressed in the pancreas tumor tissue	Unknown
96	Overexpressed in the pancreas tumor tissue	Unknown
98	Overexpressed in the pancreas tumor tissue	Unknown
99	Overexpressed in the pancreas tumor tissue	F1FO-type ATPase subunit d
100	Overexpressed in the pancreas tumor tissue	Unknown
101	Overexpressed in the pancreas tumor tissue	Human homolog to M. musculus SIK similar protein

102	Overexpressed in the pancreas tumor tissue	Unknown
103	Overexpressed in the pancreas tumor tissue	Human DNA sequence from clone 506
104	Overexpressed in the pancreas tumor tissue	MSJ-1
105	Overexpressed in the pancreas tumor tissue	Unknown
106	Overexpressed in the pancreas tumor tissue	Unknown
107	Overexpressed in the pancreas tumor tissue	Unknown
108	Overexpressed in the pancreas tumor tissue	Beta-galactoside alpha-2,6- sialyltransferase
109	Overexpressed in the pancreas tumor tissue	NHERF-2
110	Overexpressed in the pancreas tumor tissue	Unknown
111	Overexpressed in the pancreas tumor tissue	High mobility group protein
112	Overexpressed in the pancreas tumor tissue	Multi PDZ domain protein

113	Overexpressed in the pancreas tumor tissue	Unknown
114	Overexpressed in the pancreas tumor tissue	Unknown
115	Overexpressed in the pancreas tumor tissue	Unknown
116	Overexpressed in the pancreas tumor tissue	Unknown
117	Overexpressed in the pancreas tumor tissue	Unknown
118	Overexpressed in the pancreas tumor tissue	Unknown
119	Overexpressed in the pancreas tumor tissue	Unknown
120	Overexpressed in the pancreas tumor tissue	Unknown
123	Overexpressed in the pancreas tumor tissue	Unknown
124	Overexpressed in the pancreas tumor tissue	Unknown
125	Overexpressed in the pancreas tumor tissue	Unknown

126	Overexpressed in the pancreas tumor tissue	Unknown
127	Overexpressed in the pancreas tumor tissue	Unknown
128	Overexpressed in the pancreas tumor tissue	LBP-1a
129	Overexpressed in the pancreas tumor tissue	Unknown
130	Overexpressed in the pancreas tumor tissue	Unknown
131	Overexpressed in the pancreas tumor tissue	Unknown
132	Overexpressed in the pancreas tumor tissue	Unknown
133	Overexpressed in the pancreas tumor tissue	Unknown
134	Overexpressed in the pancreas tumor tissue	Unknown
135	Overexpressed in the pancreas tumor tissue	Unknown
136	Overexpressed in the pancreas tumor tissue	Unknown

137	Overexpressed in the pancreas tumor tissue	Unknown
138	Overexpressed in the pancreas tumor tissue	Unknown
139	Overexpressed in the pancreas tumor tissue	Unknown
140	Overexpressed in the pancreas tumor tissue	Unknown
142	Overexpressed in the pancreas tumor tissue	Unknown
143	Overexpressed in the pancreas tumor tissue	Unknown
144	Overexpressed in the pancreas tumor tissue	Unknown
145	Overexpressed in the pancreas tumor tissue	Homo sapiens mRNA for putatively prenylated protein
146	Overexpressed in the pancreas tumor tissue	TFG
147	Overexpressed in the pancreas tumor tissue	MLN50
148	Overexpressed in the pancreas tumor tissue	HLA-F

149	Overexpressed in the pancreas tumor tissue	Adenylate cyclase inhibiting GTP- binding protein
151	Overexpressed in the pancreas tumor tissue	AHNAK
153	Overexpressed in the pancreas tumor tissue	hPG1
154	Overexpressed in the pancreas tumor tissue	Mac-2 binding protein
155	Overexpressed in the pancreas tumor tissue	BRG1
156	Overexpressed in the pancreas tumor tissue	Gry-rbp
157	Overexpressed in the pancreas tumor tissue	NC2 alpha subunit
597	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 7
598	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 25
599	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 28
600	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 32

601	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 35
602	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 44
603	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 56
604	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 57
605	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 61
606	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 63
607	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 67
608	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 69
609	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 72
610	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 82
611	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 93

612	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 94
613	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 95
614	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 108
615	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 111
616	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 113
617	Overexpressed in the pancreas tumor tissue	Lengthening to Seq. ID No: 130

Sequenz ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker
1	In Pankreasstumorgewebe überexprimiert	unbekannt	AP_endonuclease1	Xp11.22	AFM106xa3 - SHGC-32184
2	In Pankreasstumorgewebe überexprimiert	unbekannt	rrm; PRO_RICH		
3	In Pankreasstumorgewebe überexprimiert	Humanes Homolog zu M. musculus chromaffin granule ATPase II		3p14.1-p21.1	SHGC-36252 - AFMb318yf1
4	In Pankreasstumorgewebe überexprimiert	unbekannt		14q32.13-q32.31	D14S78 - D14S292
5	In Pankreasstumorgewebe überexprimiert	HMG-1	PRO_RICH; HMG; NLS_BP		
6	In Pankreasstumorgewebe überexprimiert	NY-CO-41			
7	In Pankreasstumorgewebe überexprimiert	unbekannt	PRO_RICH	19p13.3	WI-6480
8	In Pankreasstumorgewebe überexprimiert	Humanes Homolog zu M. musculus GOB-4		7p21.3	AFMb355wg1 - SHGC-17250
9	In Pankreasstumorgewebe überexprimiert	Humanes Homolog zu B. taurus epsilon-COP			
10	In Pankreasstumorgewebe überexprimiert	Pyrophosphatase	Pyrophosphatase	4q23-q26	D4S1572 - D4S1571
11	In Pankreasstumorgewebe überexprimiert	unbekannt		9q34.2,3	D9S158
12	In Pankreasstumorgewebe überexprimiert	Humanes Homolog zu X. laevis dependent RNA helicase	DEAD; helicase_C	5q34-q351.	D5S498-D5S408
13	In Pankreasstumorgewebe überexprimiert	unbekannt	PRO_RICH	8p23.1	D8S277-D8S503
14	In Pankreasstumorgewebe überexprimiert	unbekannt	PRO_RICH; NLS_BP	9q34.13-q34.2	D9S1818-D9S158
15	In Pankreasstumorgewebe überexprimiert	unbekannt		10q21.3-q22.1	SHGC-30283
16	In Pankreasstumorgewebe überexprimiert	unbekannt			
17	In Pankreasstumorgewebe überexprimiert	unbekannt		15q23	D15S114 - D15S1329
18	In Pankreasstumorgewebe überexprimiert	unbekannt		11p11.2-q13.1	D11S1368 - SHGC-31731

Sequenz ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker
19	In Pankreastumorgewebe überexprimiert	unbekannt		5q34	
20	In Pankreastumorgewebe überexprimiert	unbekannt		14q31.3-q32.11	AFMa116zf5 - D14S968
21	In Pankreastumorgewebe überexprimiert	unbekannt	EGF;	11q13.1-q13.4	D11S913 - D11S951E
22	In Pankreastumorgewebe überexprimiert	unbekannt		1p36.13	SHGC-52575
23	In Pankreastumorgewebe überexprimiert	unbekannt	lactamase_B	12q24.22-q24.23	AFMa225xe5 - SHGC-10488
24	In Pankreastumorgewebe überexprimiert	unbekannt	ESTERASE;	3p21.1-p21.2	SHGC-14816 - WI-7113
25	In Pankreastumorgewebe überexprimiert	unbekannt			
26	In Pankreastumorgewebe überexprimiert	unbekannt			
27	In Pankreastumorgewebe überexprimiert	unbekannt		11q13.1.q13.4	D11S913-D11S1337
28	In Pankreastumorgewebe überexprimiert	unbekannt			
29	In Pankreastumorgewebe überexprimiert	unbekannt		10q23.1	SHGC-37613 - AFM029XH12
30	In Pankreastumorgewebe überexprimiert	unbekannt		7q36.2-q36.3	
31	In Pankreastumorgewebe überexprimiert	unbekannt			
32	In Pankreastumorgewebe überexprimiert	unbekannt		7p22.3-p22.1	D7S2477 - D7S517
33	In Pankreastumorgewebe überexprimiert	unbekannt			
34	In Pankreastumorgewebe überexprimiert	unbekannt			
35	In Pankreastumorgewebe überexprimiert	unbekannt		12p11.23-p13.11	D12S1629 - D12S1922
36	In Pankreastumorgewebe überexprimiert	unbekannt			
37	In Pankreastumorgewebe überexprimiert	Humanes Homolog zu M. musculus NIK	PRO_RICH; ROM_MOTIF; CNH		

Sequenz ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker
38	In Pankreasstumorgewebe überexprimiert	Humanes Homolog zu molybdoterin biosynthesis MOEB protein	ThIF_family;	3q23	
39	In Pankreasstumorgewebe überexprimiert	unbekannt		22q13.2-q13.32	IB1149 - D22S270
40	In Pankreasstumorgewebe überexprimiert	unbekannt		7q33-q35	WI-9353
41	In Pankreasstumorgewebe überexprimiert	unbekannt		11q22.3-q23.2	D11S1347 - D11S908
42	In Pankreasstumorgewebe überexprimiert	Fas-ligand associated factor 3	SH3; PRO_RICH		
43	In Pankreasstumorgewebe überexprimiert	Humanes Homolog zu M. musculus SH3P7	cofilin_ADF; SH3	7p12.2-p13	D7S519 - D7S506
44	In Pankreasstumorgewebe überexprimiert	Humanes Homolog zu C. elegans FER-1	PRO_RICH; PRO_RICH; C2_DOMAIN_2	10q23.1	D10S583; D10S185
45	In Pankreasstumorgewebe überexprimiert	Humanes Homolog zu C. griseus ars2		7q22.1	sWSS3840
46	In Pankreasstumorgewebe überexprimiert	Humanes Homolog zu einem man(9)-alpha-mannosidase ähnlichen Protein aus C. elegans		9	SHGC-37250
47	In Pankreasstumorgewebe überexprimiert	JM4		Xp21.1-Xp11.23	SHGC-17255 - SHGC-37390
48	In Pankreasstumorgewebe überexprimiert	Homolog zu cyclin C (CCNC)	PRO_RICH		
49	In Pankreasstumorgewebe überexprimiert	Homolog zu VAMP associated protein of 33kDa		20q12-q13.33	
50	In Pankreasstumorgewebe überexprimiert	Homolog zu Prepromultimerin	PRO_RICH	10q23.1	D10S564 - SHGC-15188
51	In Pankreasstumorgewebe überexprimiert	unbekannt		3p21.31-p21.1	AFM273ve9 - SHGC-30574
52	In Pankreasstumorgewebe überexprimiert	Homolog zu Fructose-1,6-biphosphalase		9q22.2	AFM212yb4 - WI-1164
53	In Pankreasstumorgewebe überexprimiert	unbekannt	PRO_RICH		
54	In Pankreasstumorgewebe überexprimiert	Hic-5	LIM	16p11.2	SHGC-36123 - SHGC-5949
55	In Pankreasstumorgewebe überexprimiert	unbekannt		1q21.2-q21.3	D1S305-D1S606

Sequenz ID No:	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker
56	In Pankreastumorgewebe überexprimiert	Polymeric immunoglobulin receptor	Ig	1q32.2-q21.3	SHGC-11228; D1S456-D1S2891
57	In Pankreastumorgewebe überexprimiert	Humanes Homolog zu H beta 58		11q23.2-q25	D11S1320 - D11S968
58	In Pankreastumorgewebe überexprimiert	Humanes Homolog zu R. norvegicus TIP49	AAA	3q21.3-q22.1	SHGC-31856
59	In Pankreastumorgewebe überexprimiert	Humanes Homolog zu R. norvegicus ABP-7		2q11.2	
60	In Pankreastumorgewebe überexprimiert	Aggrin	laminin_G; EGF		
61	In Pankreastumorgewebe überexprimiert	Triose-phosphate isomerase	TIM	12q24.33	D12S367; WI-5272
63	In Pankreastumorgewebe überexprimiert	Humanes Homolog zu M. musculus polymerase I-transcript release factor	PRO_RICH	17q11.2-q21.31	D17S800 - D17S791
64	In Pankreastumorgewebe überexprimiert	Humanes Homolog zu M. musculus AP19	Clat_adaptor_s	Xp22.33-p22.13	
65	In Pankreastumorgewebe überexprimiert	Homolog zu Ras inhibitor			
66	In Pankreastumorgewebe überexprimiert	unbekannt			
67	In Pankreastumorgewebe überexprimiert	Humanes Homolog zu S. pombe POP3	WD40_REGION	16p13.3	WI-7742
68	In Pankreastumorgewebe überexprimiert	unbekannt	PRO_RICH;	8p12	
69	In Pankreastumorgewebe überexprimiert	unbekannt		10q23.31-q23.32	Z38397
70	In Pankreastumorgewebe überexprimiert	unbekannt			
71	In Pankreastumorgewebe überexprimiert	Homolog zu APRIL	TNF; PRO_RICH	17p13.2	SHGC-31356 - SHGC-31370
72	In Pankreastumorgewebe überexprimiert	unbekannt	PRO_RICH	9p24.1-p23	D9S178 - D9S286
73	In Pankreastumorgewebe überexprimiert	unbekannt		3p21.31-p21.1	SHGC-31529
74	In Pankreastumorgewebe überexprimiert	SH3 domain binding glutamic acid-rich-like protein		Xp13.1-p22.1	SHGC-34549; DXS983-DXS995
75	In Pankreastumorgewebe überexprimiert	unbekannt		16p12.3-q12.1	D16S401 - D16S411

Sequenz ID No.	Expression	Funktion	Module	Cylogenetische Lokalisation	Nächster Marker
76	In Pankreasstomorgewebe überexprimiert	KE04p	PRO_RICH	10q23.31-q24.1	SGC32598; D10S198-D10S192
77	In Pankreasstomorgewebe überexprimiert	unbekannt		5q23.3-q31.1	TIGR-A002114; D5S396-D5S2119
78	In Pankreasstomorgewebe überexprimiert	unbekannt			
79	In Pankreasstomorgewebe überexprimiert	unbekannt	PRO_RICH		
80	In Pankreasstomorgewebe überexprimiert	Humanes Homolog zu M. musculus cell surface antigen 114/A10		3q12.3-q22.3	WI-16550; D3S1267 - D3S1269
81	In Pankreasstomorgewebe überexprimiert	Humanes Homolog zu R. norvegicus RNH-1/14-3-3	14-3-3	20q13.12-q13.2	siSG3015; D20S96 - D20S119
82	In Pankreasstomorgewebe überexprimiert	unbekannt		20q12	SHGC-5757; nih2203 - WI-7121
83	In Pankreasstomorgewebe überexprimiert	unbekannt		8q23.1-q24.23	WI-10125; D8S263 - D8S284
84	In Pankreasstomorgewebe überexprimiert	unbekannt		9q34.11-q34.12	SGC34869; D9S260 - D9S159
85	In Pankreasstomorgewebe überexprimiert	hD54		20q13.33	SHGC-3176; SHGC-9476 - SHGC-9199
86	In Pankreasstomorgewebe überexprimiert	unbekannt		21q22.12-q22.13	TIGR-A008B34; D21S1254 - D21S1252
87	In Pankreasstomorgewebe überexprimiert	Humanes Homolog zu S. pombe TPR	TPR_REGION; TPR_REPEAT		
88	In Pankreasstomorgewebe überexprimiert	Humanes Homolog zu M. musculus seizure-related mRNA	PRO_RICH	15q22.2-q22.31	WI-5241; WI-7454
89	In Pankreasstomorgewebe überexprimiert	Human KIP2 gene for Cdk-inhibitor p57KIP2 Homolog			
90	In Pankreasstomorgewebe überexprimiert	sFRP-2			
91	In Pankreasstomorgewebe überexprimiert	Homolog zu Lung Carbonyl Reductase	PRO_RICH; FZ_DOMAIN; NETRIN_CT	4q31.3	SHGC-1050; WI-15550 - D4S1046
92	In Pankreasstomorgewebe überexprimiert	Humanes Homolog zu C. elegans MSR4 like protein	adh_short	17	D17S784, n.r. (117 cM)
93	In Pankreasstomorgewebe überexprimiert	unbekannt	mito_carr	8p22-p12	siSG8989; D8S298 - D8S505
94	In Pankreasstomorgewebe überexprimiert	unbekannt			
95	In Pankreasstomorgewebe überexprimiert	unbekannt	Fork_head	3p14.1	D3S1566; CHLC.GATA52H09

Sequenz ID No:	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker
96	In Pankreastumorgewebe überexprimiert	unbekannt	C2	12q13.12-q13.13	WI-7760
98	In Pankreastumorgewebe überexprimiert	unbekannt		1q32.2	SHGC-11228; SHGC-36215 - SHGC-12033
99	In Pankreastumorgewebe überexprimiert	F1FO-type ATPase subunit d			
100	In Pankreastumorgewebe überexprimiert	unbekannt			
101	In Pankreastumorgewebe überexprimiert	Humanes Homolog zu M. musculus SIK similar protein	NLS_BP	16q24.1-q24.2	CHLC.GATA71F09
102	In Pankreastumorgewebe überexprimiert	unbekannt			
103	In Pankreastumorgewebe überexprimiert	Human DNA sequence from clone 5O6		22q13.1	SHGC-2785; IB342 - SHGC-37043
104	In Pankreastumorgewebe überexprimiert	MSJ-1	DnaJ	11q13.2-q13.4	AFMa190xd9
105	In Pankreastumorgewebe überexprimiert	unbekannt	PDZ	Xq12.2	CHLC.GGATA64D08; DXS983
106	In Pankreastumorgewebe überexprimiert	unbekannt	UPF0034		
107	In Pankreastumorgewebe überexprimiert	unbekannt			
108	In Pankreastumorgewebe überexprimiert	Beta-galactosid alpha-2,6-sialyltransferase	Sialyltransf; PRO_RICH	3q26.33-3q28	D3S1602-D3S1580
109	In Pankreastumorgewebe überexprimiert	NHERF-2	PDZ	16q22.1-q23.1	SHGC-11460
110	In Pankreastumorgewebe überexprimiert	unbekannt		6p21.31-p21.2	
111	In Pankreastumorgewebe überexprimiert	high mobility group protein	HMG_box	Xq28	
112	In Pankreastumorgewebe überexprimiert	Multi PDZ domain protein	NLS_BP; PDZ	9p23-p21.3	SHGC-32204; WI-7091 - SHGC-3971
113	In Pankreastumorgewebe überexprimiert	unbekannt	G-beta	11q12	
114	In Pankreastumorgewebe überexprimiert	unbekannt	NLS_BP; PRO_RICH	?	SHGC-2325; SHGC-36512
115	In Pankreastumorgewebe überexprimiert	unbekannt		1p36.11-p36.13	

Sequenz ID No.	Expression	Funktion	Module	Cylogenetische Lokalisation	Nächster Marker
116	In Pankreasstumorgewebe überexprimiert	unbekannt		9q34.11-q34.2	AFMb001ve9; AFM122xf4 - SHGC-2757
117	In Pankreasstumorgewebe überexprimiert	unbekannt		17q21.31-q22	SGC32559; D17S797- D17S788
118	In Pankreasstumorgewebe überexprimiert	unbekannt	PRO_RICH;	3q13.33-q23	WI-9557; D3S1589 - D3S1292
119	In Pankreasstumorgewebe überexprimiert	unbekannt		11p12-q13.1	D11S1357-D11S1765
120	In Pankreasstumorgewebe überexprimiert	unbekannt		5q34-q35.1	EST00061; SHGC-11657 - UT5261
123	In Pankreasstumorgewebe überexprimiert	unbekannt		19q13.2-q13.33	WI-11704; D19S219- D19S418
124	In Pankreasstumorgewebe überexprimiert	unbekannt		11	
125	In Pankreasstumorgewebe überexprimiert	unbekannt		Xq12.2	
126	In Pankreasstumorgewebe überexprimiert	unbekannt		20q11.21-q12	TIGR-A001Z33; D20S195- D20S107
127	In Pankreasstumorgewebe überexprimiert	unbekannt		10q25.3	CHLC.GATA71C09
128	In Pankreasstumorgewebe überexprimiert	LBP-1a	PRO_RICH;	3p22.3	GATA8A06
129	In Pankreasstumorgewebe überexprimiert	unbekannt		17q21.32-q22	SHGC-31935; NIB1385 - SHGC-30378
130	In Pankreasstumorgewebe überexprimiert	unbekannt			
131	In Pankreasstumorgewebe überexprimiert	unbekannt		13	SHGC-6203
132	In Pankreasstumorgewebe überexprimiert	unbekannt		7p13	AFM288vb5; D7S679 - D7S2561
133	In Pankreasstumorgewebe überexprimiert	unbekannt		14q24.2-q24.3	WI-7648; D14S946
134	In Pankreasstumorgewebe überexprimiert	unbekannt		19p13.3	SHGC-1247
135	In Pankreasstumorgewebe überexprimiert	unbekannt		1p34.3	SHGC-6708; D1S432 - D1S2540
136	In Pankreasstumorgewebe überexprimiert	unbekannt	PRO_RICH;	5q32-q33.1	

Sequenz ID No.	Expression	Funktion	Module	Cyogenetische Lokalisation	Nächster Marker
137	In Pankreasstumorgewebe überexprimiert	unbekannt		8q21.11 =pct141	SHGC-53839/AFM172xf10
138	In Pankreasstumorgewebe überexprimiert	unbekannt			
139	In Pankreasstumorgewebe überexprimiert	unbekannt		11q14.3-q22.2	
140	In Pankreasstumorgewebe überexprimiert	unbekannt	GLOBIN	Xq22.3-q25	SHGC-32433
142	In Pankreasstumorgewebe überexprimiert	unbekannt		17p13.2-p12	siSG4857; D17S796 - D17S960
143	In Pankreasstumorgewebe überexprimiert	unbekannt		16q12.2-q13	AFMa061yb5
144	In Pankreasstumorgewebe überexprimiert	unbekannt		2p24.1	AFM200ZC11; AFM207vo7 - SHGC-30375
145	In Pankreasstumorgewebe überexprimiert	Homo sapiens mRNA for putatively prenylated protein	PRO_RICH;	Xq25-q27.3	WI-6213; WI-5285
146	In Pankreasstumorgewebe überexprimiert	TFG		6p21.2	SHGC-31456; SHGC-10980 - SHGC-16715
147	In Pankreasstumorgewebe überexprimiert	MLN50	LIM_DOMAIN_2; SH3	17q11.2	SHGC-36242; SHGC-3073 - AFMa302yb5
148	In Pankreasstumorgewebe überexprimiert	HLA-F	MHC_I; PRO_RICH	6p21.31	SHGC-4087; SHGC-10115 - SHGC-17229
149	In Pankreasstumorgewebe überexprimiert	Adenylate cyclase inhibiting GTP-binding protein	G-alphaarf	12p12.3	SHGC-2112; D12S308 - D12S1832
151	In Pankreasstumorgewebe überexprimiert	AHNAK	PRO_RICH; RICIN_B_LLECTIN	11p11.2-q13.1	SHGC-15940; D11S1368 - SHGC-31731
153	In Pankreasstumorgewebe überexprimiert	hPGI	LRR	Xq28	SHGC-35272
154	In Pankreasstumorgewebe überexprimiert	Mac-2 binding protein	PRO_RICH	17	SHGC-11286; SHGC-33563 - AFM163yg1
155	In Pankreasstumorgewebe überexprimiert	BRG1		19p13.2-p13.3	SHGC-9937; D19S221 - D19S226
156	In Pankreasstumorgewebe überexprimiert	Gry-fbp	RBD; PRO_RICH; rrm	20p13-p12.3	SHGC-56771; D20S816 - D20S779
157	In Pankreasstumorgewebe überexprimiert	NC2 alpha subunit	HIST_TAF	11q13.1-q13.3	SHGC-1320; D11S951E - SHGC-10519

Sequenz ID No:	Expression	Funktion	Module	Cylogenetische Lokalisation	Nächster Marker
597	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 7			
598	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 25			
599	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 28			
600	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 32			
601	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 35			
602	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 44			
603	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 56			
604	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 57			
605	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 61			
606	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 63			
607	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 67			
608	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 69			
609	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 72			
610	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 82			
611	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 93			
612	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 94			
613	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 95			
614	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 108			
615	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 111			

Sequenz ID No:	Expression	Funktion	Cytogenetische Lokalisation	Nächster Marker
616	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 113		
617	In Pankreastumorgewebe überexprimiert	Verlängerung zu Seq ID No: 130		

TABLE II

DNA Sequences
Seq. ID No.:

Peptide Sequences
Seq. ID No.:

1	158
	159
	160
2	161
	162
	163
3	164
	165
	166
4	167
	168
	169
5	170
	171
	172
6	173
	174
	175
7	176
	177
	178
8	179
	180
	181
9	182
	183
	184
10	185
	186
	187
11	188
	189
	190
12	191
	192
	193
13	194
	195
	196
14	197
	198
	199
15	200
	201
	202
16	203
	204
	205
17	206
	207

DNA Sequences
Seq. ID No.:
Peptide Sequences
Seq. ID No.:

18	209
	210
	211
19	212
	213
	214
20	215
	216
	217
21	218
	219
	220
22	221
	222
	223
23	224
	225
	226
24	227
	228
	229
25	230
	231
	232
26	233
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27	236
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28	239
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29	242
	243
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30	245
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	247
31	248
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	250
32	251
	252
	253
33	254
	255
	256
34	257
	258
	259

DNA Sequences
Seq. ID No.:
Peptide Sequences
Seq. ID No:

35	260
	261
	262
36	263
	264
	265
37	266
	267
	268
38	269
	270
	271
39	272
	273
	274
40	275
	276
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41	279
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42	282
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43	285
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44	288
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45	291
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46	294
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47	297
	298
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48	300
	301
	302
49	303
	304
	305
50	306
	307
	308
51	309
	310

DNA Sequences
Seq. ID No.:
Peptide Sequences
Seq. ID No.:

52	312
	313
	314
53	315
	316
	317
54	318
	319
	320
55	321
	322
	323
56	324
	325
	326
	327
57	328
	329
58	330
	331
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66	354
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67	357
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68	360
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	362
69	363
	364
	365

DNA Sequences
Seq. ID No.:
Peptide Sequences
Seq. ID No:

70	366
	367
	368
71	369
	370
	371
72	372
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73	375
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74	378
	379
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75	381
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76	384
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83	405
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83	407
84	408
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85	411
	412
	413
86	414
	415
	416

DNA Sequences
Seq. ID No.:
Peptide Sequences
Seq. ID No:

87	417
	418
	419
88	420
	421
	422
90	426
	427
	428
	429
91	430
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	432
92	433
	434
	435
93	436
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94	439
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98	451
	452
	453
	454
99	455
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100	458
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	460
101	461
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	463
102	464
	465
	466
103	467
	468
	469
104	470
	471
	472

DNA Sequences
Seq. ID No.:
Peptide Sequences
Seq. ID No:

105	473
	474
	475
106	476
	477
	478
107	479
	480
	481
108	482
	483
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109	485
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	487
110	488
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111	491
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112	494
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113	497
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114	501
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115	504
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116	507
	508
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117	510
	511
	512
118	513
	514
118	515
119	516
	517
	518
120	519
	520
	521
123	528
	529

DNA Sequences
Seq. ID No.:
Peptide Sequences
Seq. ID No:

	530
124	531
	532
	533
125	534
	535
	536
126	537
	538
	539
127	540
	541
	542
128	543
	544
	545
129	546
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130	549
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130	551
131	552
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132	555
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133	558
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134	561
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135	564
	565
	566
136	567
	568
	569
137	570
	571
	572
138	573
	574
	575
139	576
	577
	578
	579
	580
	581

DNA Sequences
Seq. ID No.:
Peptide Sequences
Seq. ID No.:

140	582
	583
	584
142	588
	589
	590
143	591
	592
	593
144	594
	595
	596
597	618
	619
598	620
	621
599	622
	623
600	624
	625
601	626
	627
602	628
	629
603	630
	631
604	632
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605	634
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606	636
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607	638
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608	640
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609	642
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610	644
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611	646
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612	648
	649
613	650
	651
614	652
	653
615	654
	655
616	656

DNA Sequences
Seq. ID No.:

Peptide Sequences
Seq. ID No:

617	657
	658
	659

The inventive nucleic acid sequences Seq. ID Nos. 1-157, 597-617 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 158-596, 618-659 are described in the following sequence protocol.

Systematic Gene Search in the Incyte LifeSeq Database

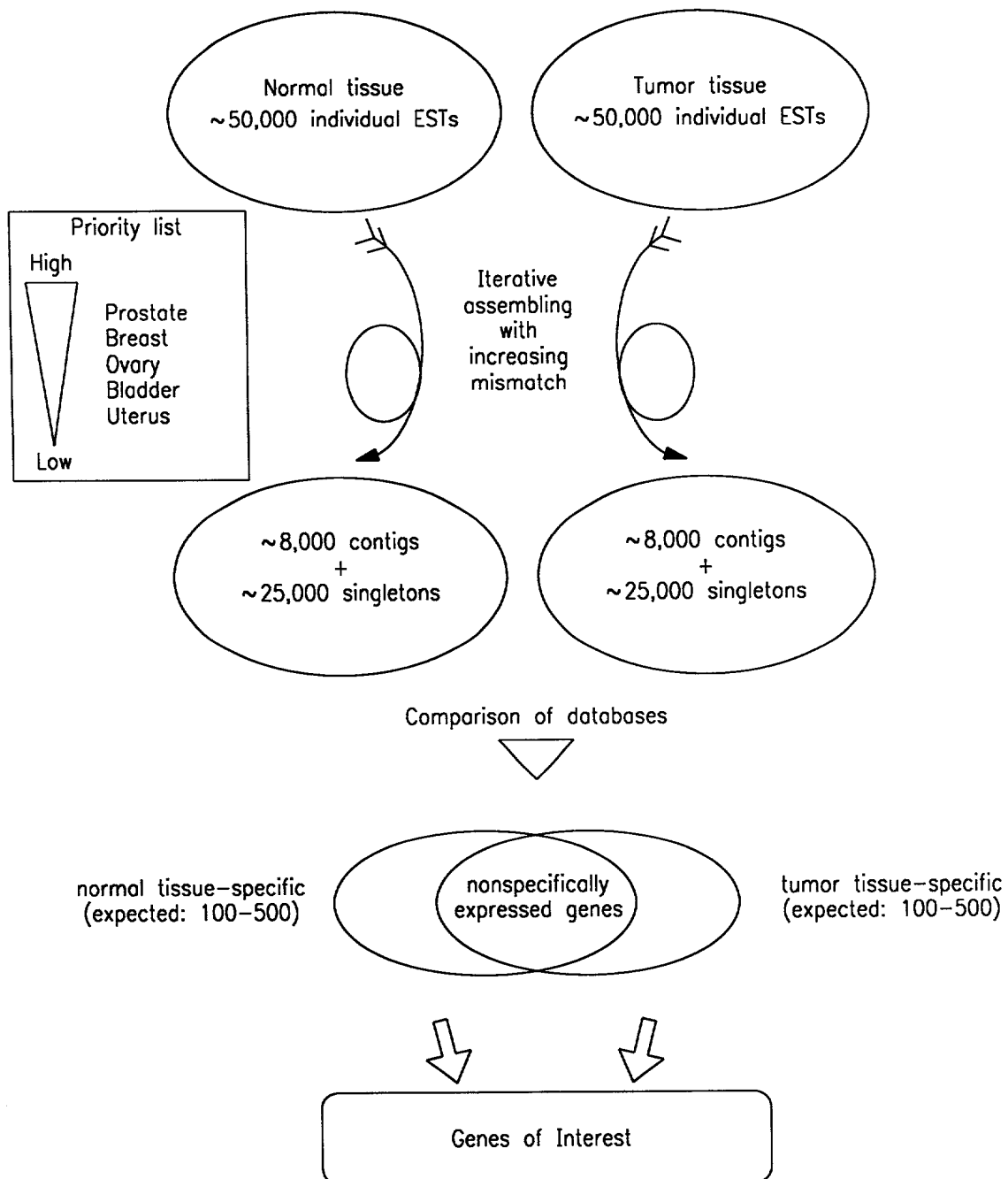


FIG. 1

Principle of EST Assembly

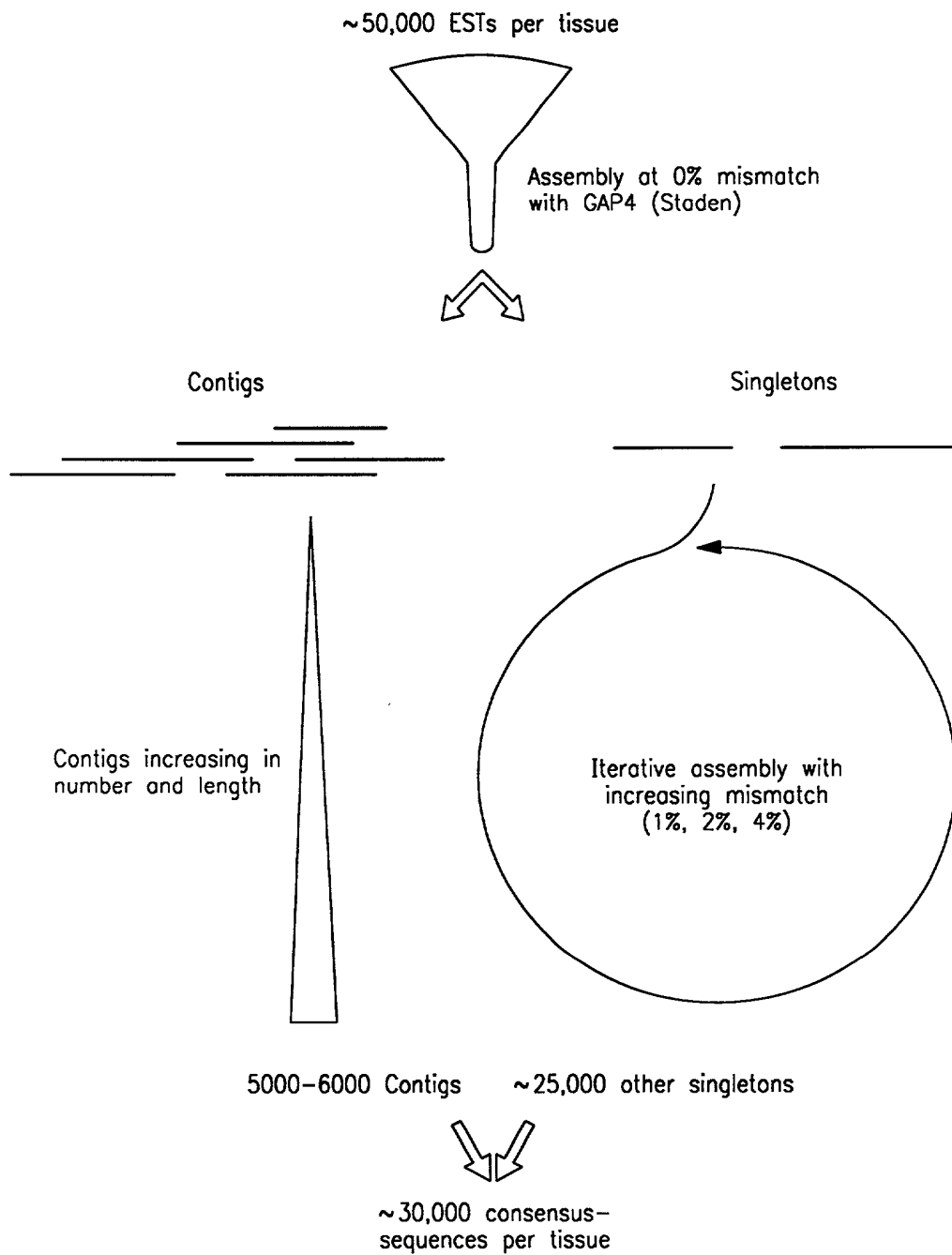


FIG. 2a

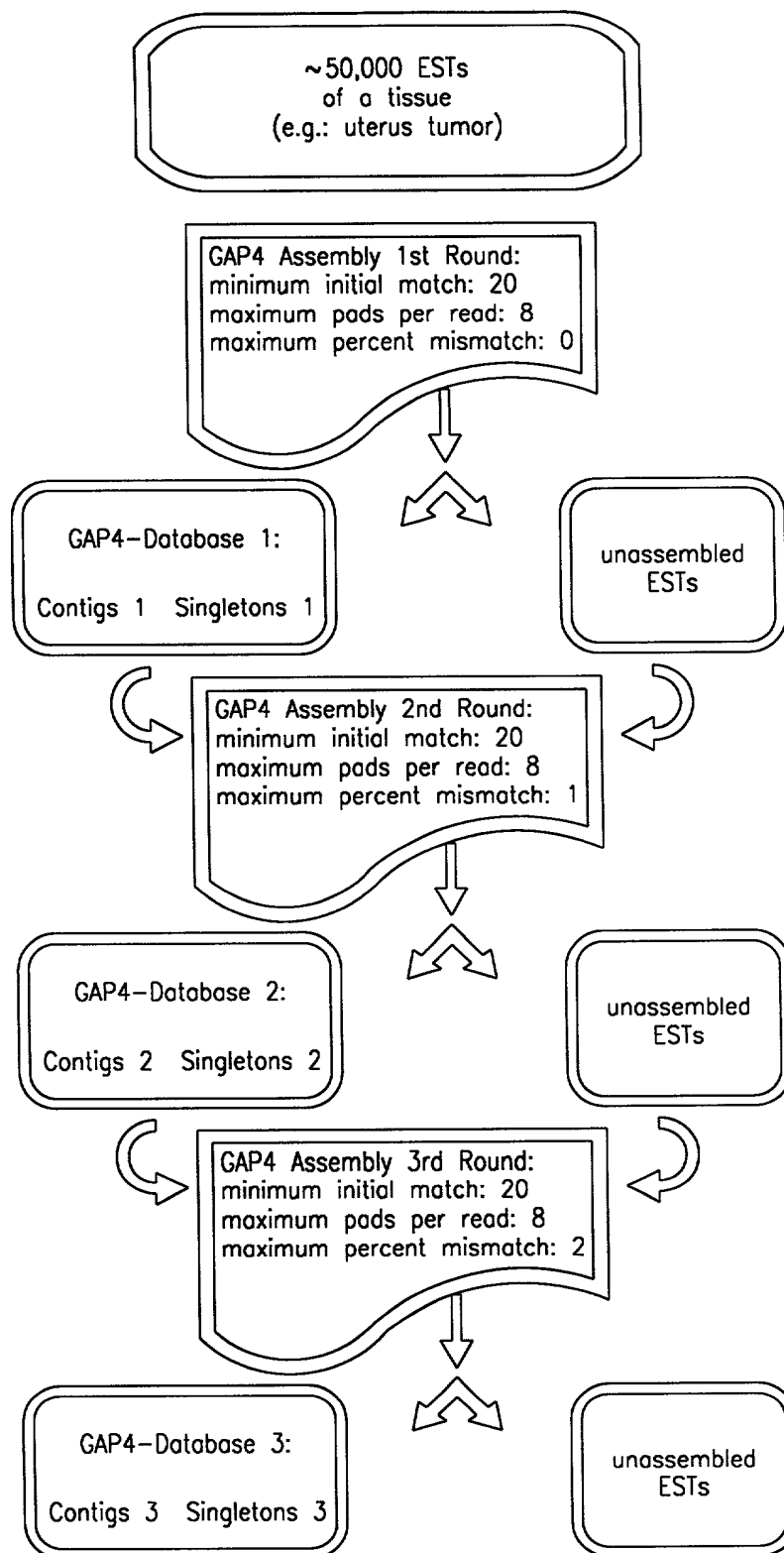


FIG. 2b-I

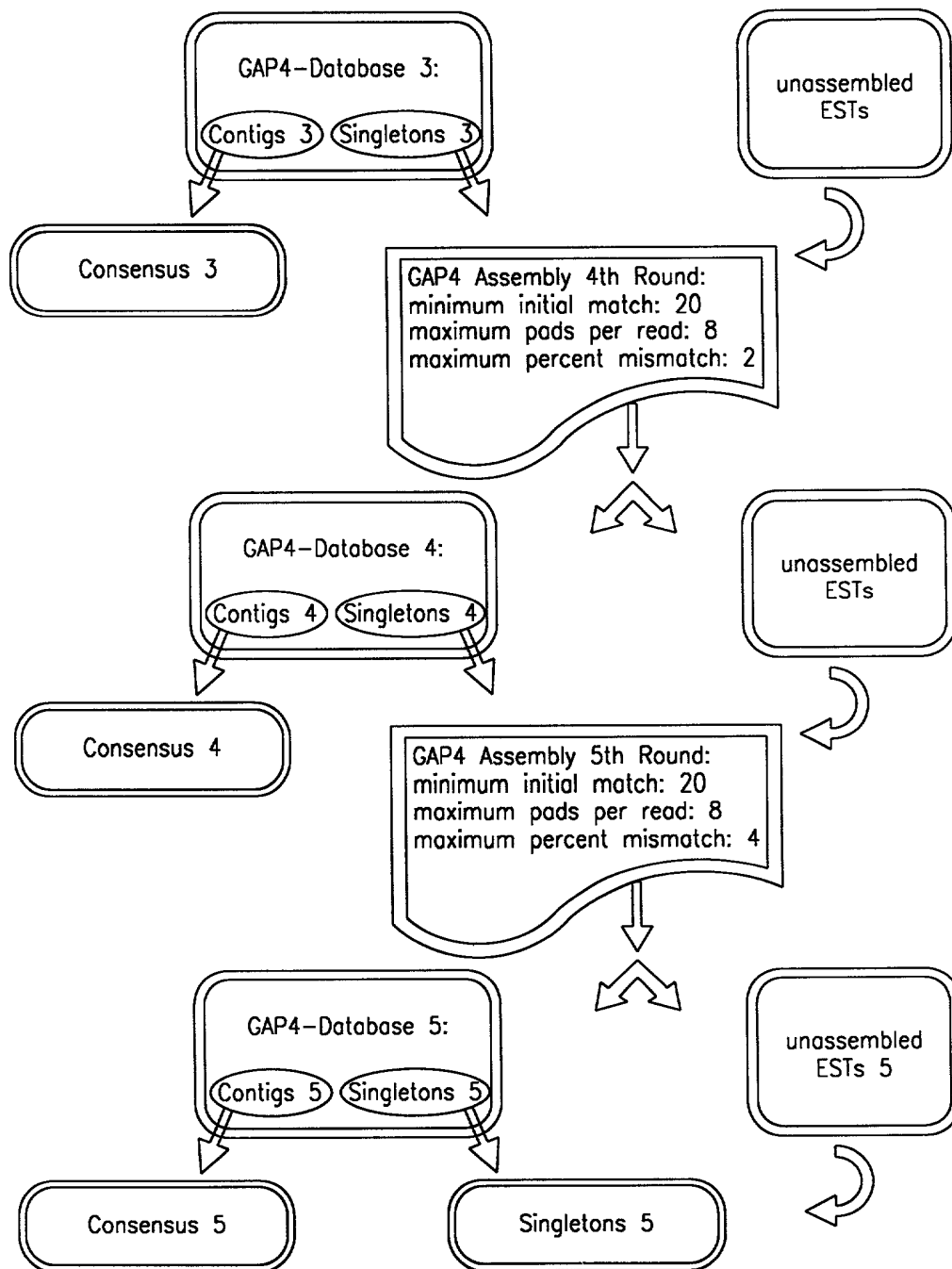


FIG. 2b-2

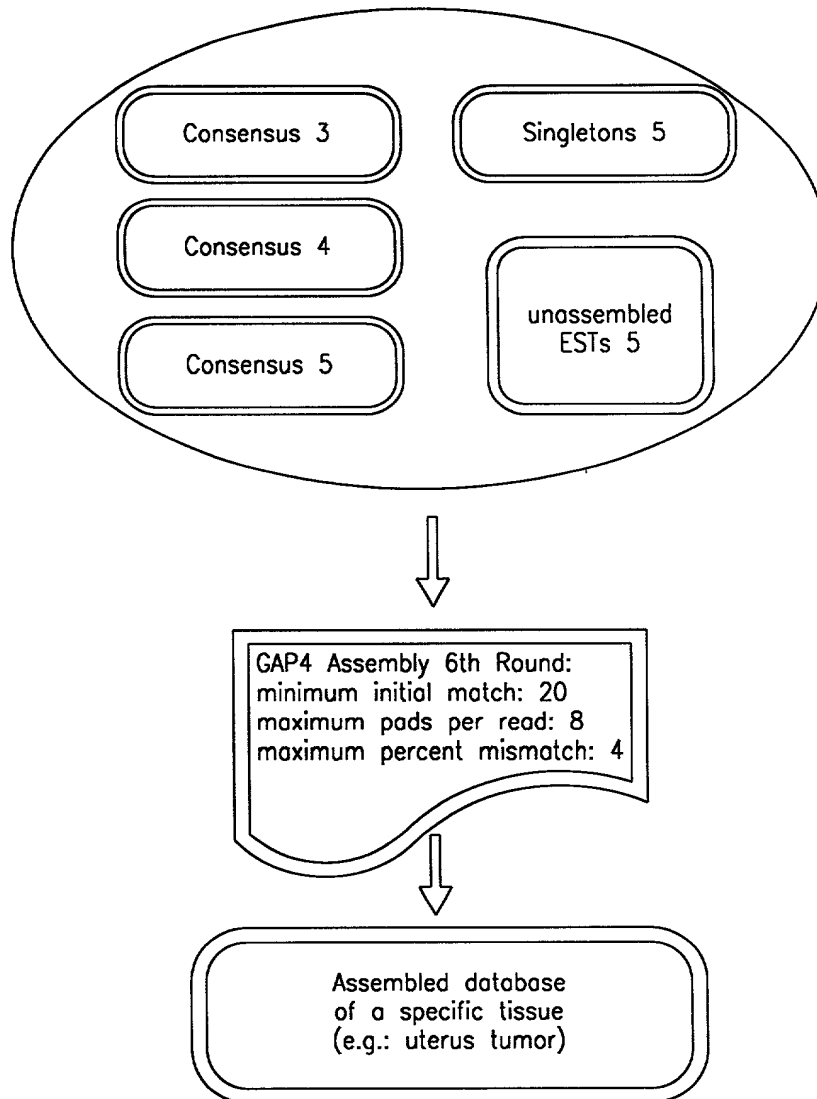


FIG. 2b-3

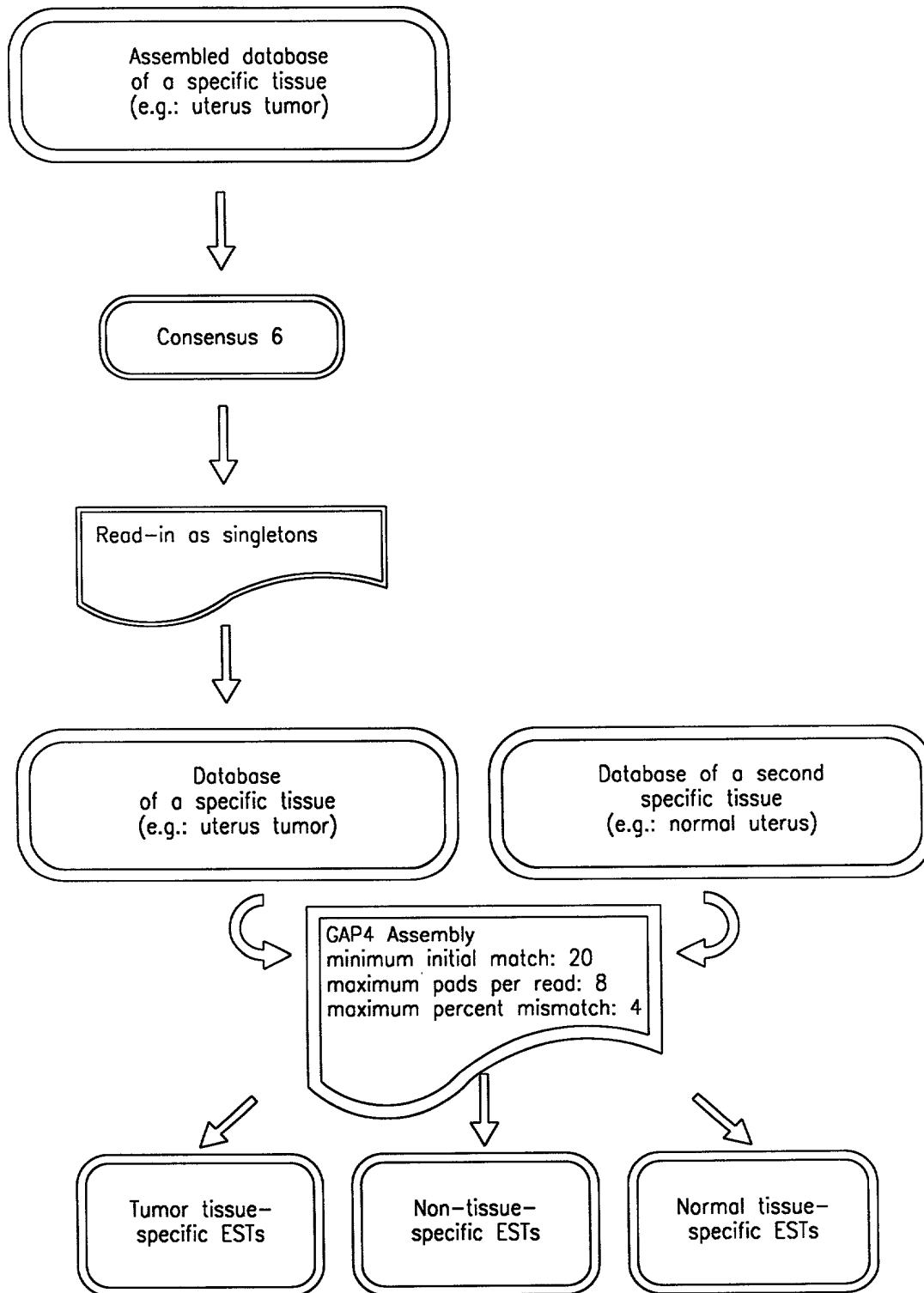


FIG. 2b-4

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
cancer tissue

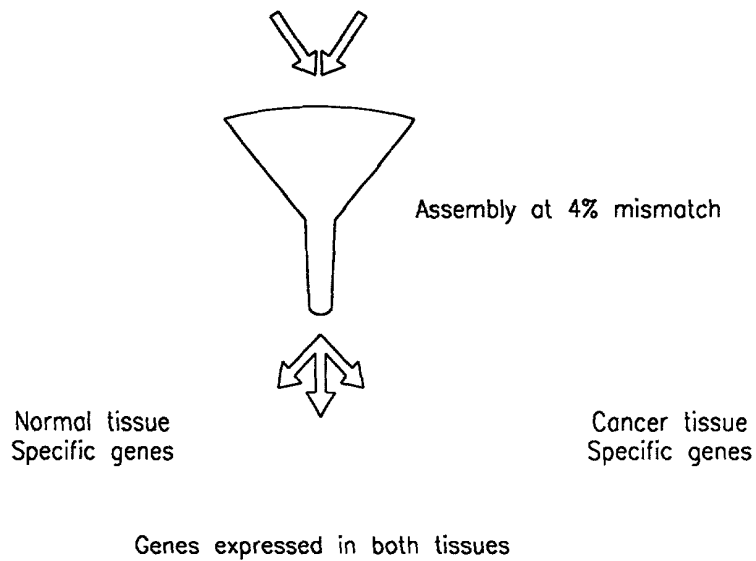


FIG. 3

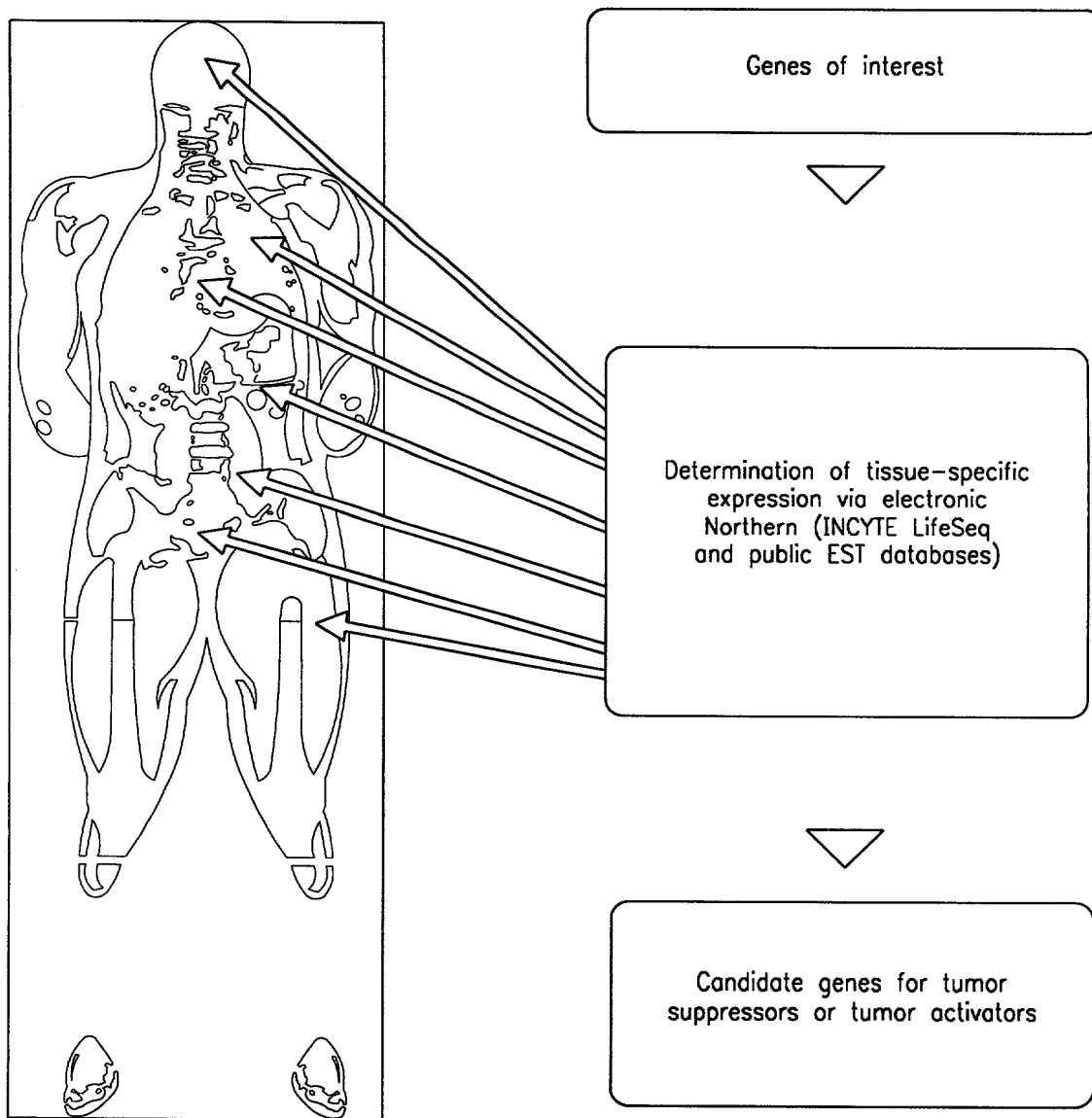


FIG. 4a

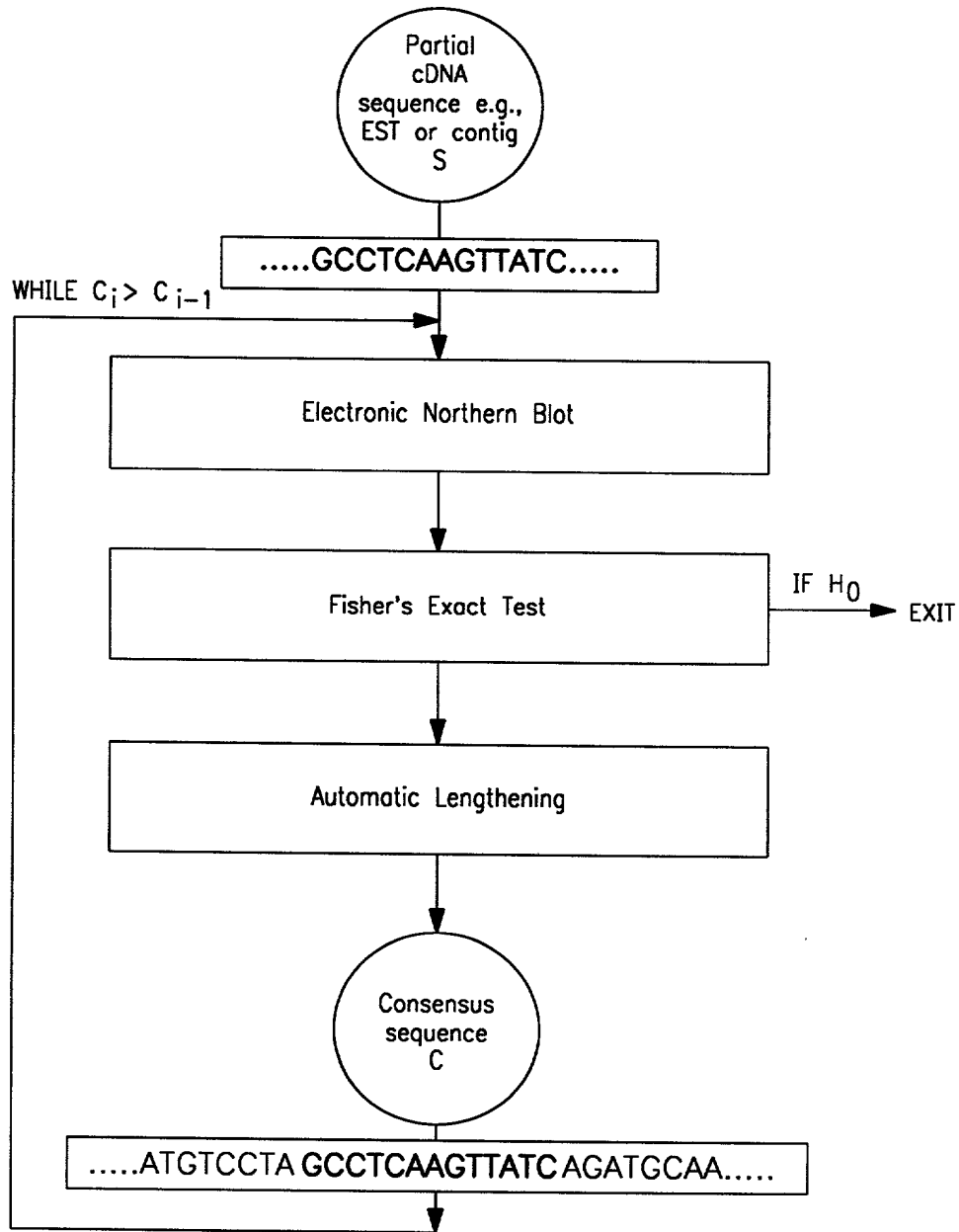


FIG. 4b

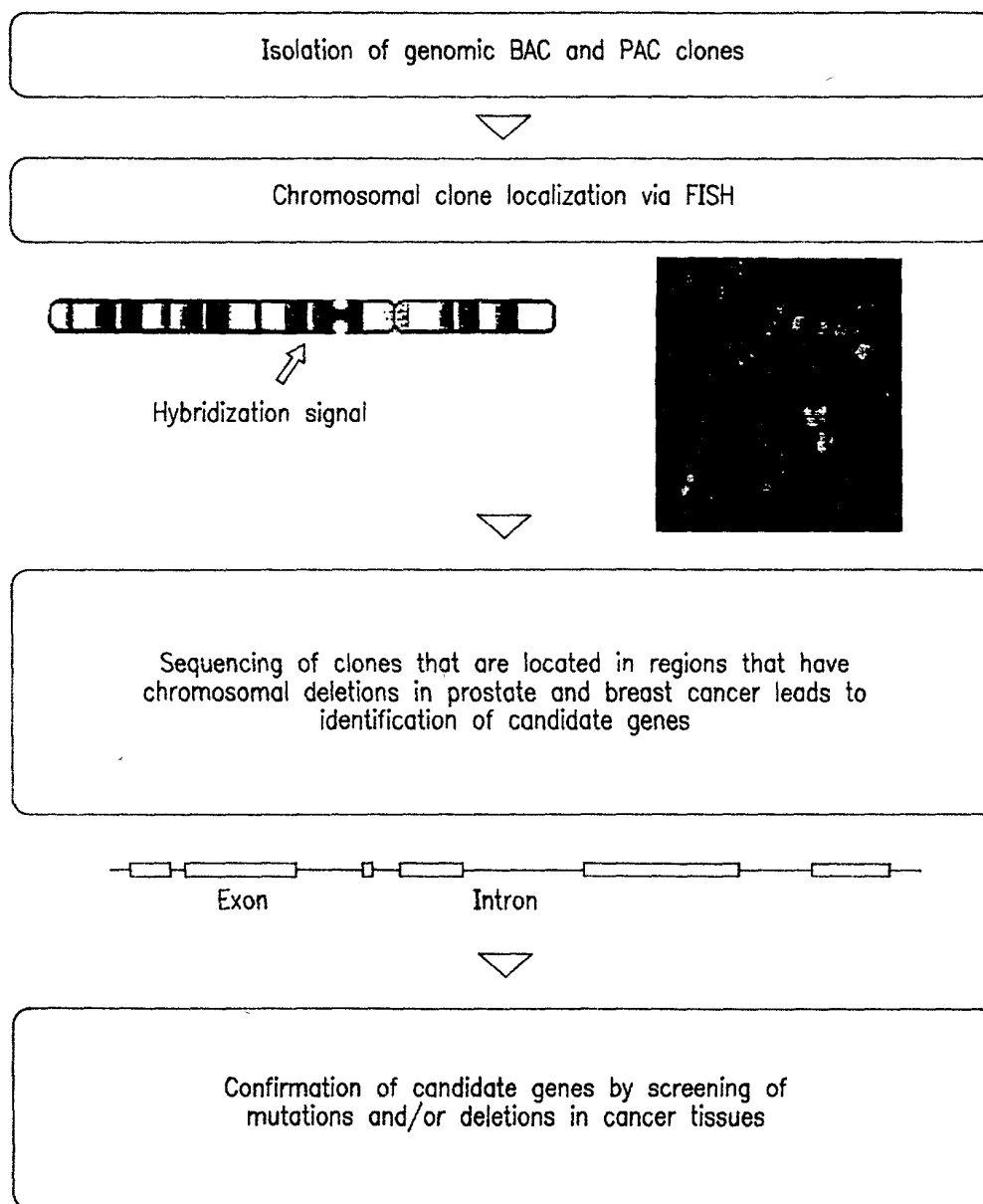


FIG. 5

Attorney Docket Number: SCH 1787**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN NUCLEIC ACID SEQUENCES OBTAINED FROM PANCREAS TUMOR TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 19 APRIL 1999 as United States Application Number or PCT International Application Number PCT/DE99/01258 and (if applicable) was amended on _____

I hereby authorize our attorneys to insert the serial number assigned to this application

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 20 190 7	GERMANY	28/04/98	YES

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

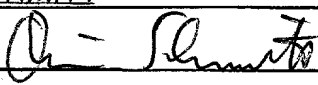
I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E. J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brion P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Catherine M. Joyce (40,668); Nancy J. Axelrod (44,014); James T. Moore (35,619); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

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TEL (703) 243-6333
FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

Full Name of sole or first inventor (given name family name)	
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Full Name of additional joint inventor (given name family name)	
Bernd HINZMANN	
Signature	Date
Residence	Citizenship
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Full Name of additional joint inventor (given name family name)	
Armin SCHMITT	
Signature 	Date October 28 2000
Residence	Citizenship
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Signature	Date
Residence	Citizenship
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Edgar DAHL	
Signature	Date
Residence	Citizenship
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Post Office Address Koppenplatz 10, D-10115 Berlin, Germany	

☐ Additional joint inventors are named on separately numbered sheets attached hereto.

Attorney Docket Number: SCH 1787**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN NUCLEIC ACID SEQUENCES OBTAINED FROM PANCREAS TUMOR TISSUE

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PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIM UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 20 190 7	GERMANY	28/04/98	YES

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PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

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I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E. J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brion P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Catherine M. Joyce (40,668); Nancy J. Axelrod (44,014); James T. Moore (35,619); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

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FAX (703) 243-6410

over

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Full Name of sole or first inventor (given name family name)	
1-00 Thomas SPECHT	
Signature <i>Thomas Specht</i>	Date 27.10.00
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Berlin Germany DEX	German
Post Office Address Grabenstrasse 14, D-12209, Berlin, Germany	
Full Name of additional joint inventor (given name family name)	
2-00 Bernd HINZMANN	
Signature <i>Bernd Hinzmann</i>	Date 27.10.00
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Berlin Germany DEX	German
Post Office Address Parkstrasse 19, D-13127 Berlin, Germany	
Full Name of additional joint inventor (given name family name)	
3-00 Armin SCHMITT	
Signature	Date
Residence	Citizenship
Berlin Germany	German
Post Office Address Laubacher Strasse 6/II, D-14197 Berlin, Germany	
Full Name of additional joint inventor (given name family name)	
4-00 Christian PILARSKY	
Signature <i>Christian Pilarsky</i>	Date 27.10.00
Residence	Citizenship
Schonfeld Germany DEX	German
Post Office Address Heinrich-Lange-Strasse 13c, D-01474 Schönfeld, Germany	
Full Name of additional joint inventor (given name family name)	
5-00 Edgar DAHL	
Signature <i>Edgar Dahl</i>	Date 27.10.2000
Residence	Citizenship
Potsdam Germany DEX	German
Post Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany	
Full Name of additional joint inventor (given name family name)	
6-00 André ROSENTHAL	
Signature <i>André Rosenthal</i>	Date 27 10 00
Residence	Citizenship
Berlin Germany DEX	German
Post Office Address Koppenplatz 10, D-10115 Berlin, Germany	

☐ Additional joint inventors are named on separately numbered sheets attached hereto.

K:\PAT\Sch\1787\Decl wpg

Sequence Protocol

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: metaGen - Gesellschaft für Genomforschung
mbH
- (B) STREET: Ihnestrass 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from
Pancreas Tumor Tissue

(iii) Number of sequences: 633

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25
(EPO)

(2) INFORMATION ON SEQ ID NO. 1:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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cttcatcgat agctaccgct gcttccaacc aaagcaggag ggggccttca cctgctgggtc 60
agcagtcact ggcgccccgcc atctcaacta tggctcccgg cttgactata ccctggggga 120

caggaccctg gtcatagaca cctttcaggc ctctttcctg ctgcctgagg tgatgggctc 180
tgaccactgc cctgtgggtg cagtcttgag tgtgtcctct gtgcctgcaa aacagtgcc 240
acctctgtgc acccgcttcc tccctgagtt tgcaggcacc cagctcaaga tccttcgctt 300
cctagtctct ctogaacaaa gtctgtgtgt ggagcagtcg acgctgcagc acaacaatca 360
aaccgggga cagacatgcc aaaacaaagc ccaagtgcgc tcaaccaggc ctgagcccag 420
tcagggttggc tctagcagag gccagaaaaa cctgaagagc tactttcagc cctcccctag 480
ctgtccccc aa gctctcctg acatagagct gcctagccta ccactgatga gcgccctcat 540
gaccccgag actccagaag agaaggcagt ggccaaagt gtgaaggggc aggccaaagac 600
ttcagaagcc aaagatgaga aggagttacg gacctattc tggaagtctg tgctggcggg 660
gccccttgcgc acacccctct gtggggggcca caggagacca tgtgtgatgc gtactgtgaa 720
gaagccagga cccaacttgg gccgcgctt ctacatgtgt gccaggcccc ggggtcctcc 780
cactgacccc tctcccggt gcaattcttc ctctggagca ggcccagctg aaccaatgga 840
ggcctgggga catctggcat ggtcaccctt gcacatgatc tgaggccagc tccccttccc 900
tgagctgctt cctgcttctc cctcaaagtc tctaccctt ctcttctctt ttaagccct 960
ctcttctctg ctttcttccc tacttagctc cttgttggtg agcttcttgt gccttaatcc 1020
tgtgaccag ccccttacac cactttccac cttctgtccc gaagtacacg gacactagct 1080
gcccagga gttgtgtgat tttaaatcac ttctgtcttt gctggaaagt gtatttgtgc 1140
ataaataaag tctgtgtatt tgtttcaaaa aaaaaaaagg ggtttgaagg 1200
gg

```

(2) INFORMATION ON SEQ ID NO. 2:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

cctccatcag ctgcgcgcgc agcggctgta tttgcggcct gtgcgagtag gcgcttgggc 60
actcagtctc cctggcgagc gacgggcaga aatctcgaac cagtggagcg cactcgtaac 120
ctggatccca gaaggtcgcg aaggcagtac cgtttcctca gcggcggact gctgcagtaa 180
gaatgtcttt tccacctcat ttgaatcgcc ctcccattgg aatcccagca ctcccaccag 240
ggatcccacc cccgcagttt ccaggatttc ctccacctgt acctccaggg accccaatga 300
ttcctgtacc aatgagcatt atggctcctg ctccaactgt cttagtacct actgtgtcta 360
tggttggaag gcatttgggc gcaagaaagg atcatccagg cttaaaggct aaagaaaatg 420
atgaaaattg tggctctact accactgttt ttggtggcaa catttccgag aaagcttcag 480
acatgcttat aagacaactc ttagctaaat gtggtttggt tttgagctgg aagagagtac 540
aagggtgcttc cggaaagctt caagccttcg gattctgtga gtacaaggag ccagaatcta 600
ccctccgtgc actcagatta ttacatgacc tgcaaattgg agagaaaaag ctactcgtaa 660
aagttgatgc aaagacaaag gcacagctgg atgaatggaa agcaaaagag aaagcttcta 720
atgggaatgc aaggccagaa actgtcacta atgacgatga agaagccttg gatgaagaaa 780
caaagaggag agatcagatg attaaagggg ctattgaagt tttaattcgt gaatactcca 840
gtgagctaaa tgccccctca caggaatctg attctcacc ccaggaagaa gaagaaggaa 900
aagaaggagg acattttccg cagatttcca gtggccccac tgatccctta tccactcatc 960
actaaggagg atataaatgc tatagaaatg gaagaagaca aaagagacct gatatctcga 1020
gagatcagca aattcagaga cacacataag aaactggaag aagagaaagg ca 1072

```

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1468 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

gcacgaggtta ttatgctgtc gtatggctcc actgcagaaa gcaaaagtaa taagactaat 60
aaaaatatca cctgagaaac ctataacatt ggctgttggg gatggtgcta atgacgtaag 120
catgatacag gaggcccatg ttggcatagg aatcatgggt aaagaaggaa gacaggctgc 180
aagaaacagt gactatgcaa tagccagatt taagttcctc tccaaattgc tttttgttca 240
tggtcatttt tattatatta gaatagctac cttgttacag tatttttttt ataagaatgt 300
gtgctttatc acacccaggt ttttatatca gttctactgt ttgttttctc agcaaacatt 360
gtatgacagc gtgtacctga ctttatacaa tatttgtttt acttccctac ctattctgat 420
atatagtctt ttggaacagc atgtagacct tcatgtgtta caaaataagc ccacccttta 480
tcgagacatt agtaaaaacc gcctcttaag tattaaaaca tttctttatt ggaccatcct 540
gggcttcagt catgccttta ttttcttttt tggatcctat ttactaatag ggaaagatac 600
atctctgctt ggaaatggcc agatgtttgg aaactggaca tttggcactt tggctctcac 660
agtcattggt attacagtca caataaagat ggctctggaa actcattttt ggacttggat 720
caaccatctc gttacctggg gatctattat attttatttt gtattttcct tgttttatgg 780
agggattctc tggccatttt tgggctccca gaatatgtat tttgtgttta ttcagctcct 840
gtcaagtggg tctgcttggg ttgccataat cctcatgggt gttacatgtc tatttcttga 900
tatcataaag aaggtctttg accgacacct ccaccctaca agtactgaaa aggcacagat 960
gtactccaac acagttgctt taagtgcga gttcatcgca ctgcagccat tgtcgagggc 1020
aaggaatcag ctgagcaaac ttagcttact gaaacaaatg caggtatcaa gtgcttggac 1080
tccatgtgct gtttcccgga aggagaagca gcgtgtgcat ctgttggaag aatgctgga 1140
cgagttatag gaagatgtag tccaaccac atcagcaggt gtgaaatctc tctaagtagc 1200
ctttgctgca gatgagtatc ctatctggaa caggatgaac ctgccgctct agataccta 1260
taaatcagca gctggtttta ccaactgaag caggaagtct gctattttatt agcactcttt 1320
ggtggtagat ttcactttgt ggctttgggg taagggtttt ttcactcaca aaggaagaga 1380
aagcaccttt gaagagactt catctaata acaaaaaatt ttgtttcata atctttcta 1440
aatgggctca gtaggagtgg gtgtatgg

```

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2331 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

cggtctgaga aaggacctct cctttttcag atgctctggca tgaggcttcc agaaacccag 60
gtttcttccag gagaaataga tgagactcct ctttccaagc caggacatga ccttgccagc 120
atggaggata aaacagagaa atggtcttcc cagcctgaag gtccacttaa attgaaagct 180
tcaagtactg atatgccatc ccagatttct gtggttaatg tggatcaact gtgggaagat 240
tctgtcctaa ctgtcaaatt ccccaaatta atggtaccaa ggttctcctt ccctgcccc 300
agctcagagg atgatgtgtt catccccact gtgagggaag tgcagtgtcc agaggccaat 360
attgatacag ccctttgtaa ggaaagtccg gggctctggg gagccagcat cctgaaggca 420
gggtgctgggg tccctgggga gcagcctgtg gaccttaacc tgcctttgga agtccccca 480
atttcaaagg tcagagtga tattcagggt gctcaggttg aaagtcaaga ggtcactata 540
cacagcatag tgacaccaga gttttagat ctctcagtac ccaggacttt ttccactcag 600
attgtgoggg aatcagagat cccacgtca gagattcaaa caccttcgta cggattttcc 660
ttattaaaag tgaaaatccc agagccccac acgcaggcta gagtgtacac aacaatgact 720
caacactcta ggactcagga gggcacagaa gaggctccca tacaagccac ccaggagta 780
gactccattt ctggagatct ccagcctgac actggagaac catttgagat gatctcttcc 840
agcgtcaatg tactgggaca gcaaacactc acatttgaag ttcttctctg ccaccagctt 900
gcagacagct gttcagatga ggagccagca gaaattcttg agtttcccc tgatgatagc 960
caagaggcaa ccacaccact ggcagatgaa ggcagggtct caaaagacaa accagaaagt 1020
aaaaaatctg gtctgtcttg gttttggctt ccaaacattg ggttttcctc ttctgttgat 1080
gagacaggtg ttgattccaa aaatgacgtc cagagatctg ctcccattca aacacagcct 1140
gaggcacgac cagaggcaga actgcctaaa aaacaggaga aggcaggctg gttccgattt 1200
cccaaattag ggttctcctc atctcctacc aagaaaagca aaagcacgca agatggggca 1260
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ctcatcagta caagagagat gcaaaaaact aagttggaaa gtaaaggcta cacacacata 1560
tggagcacc ccatccacag cacattacat ccacctcact tcacagaacg gagaacagag 1620
cagaaatgac cagaacacct ttgtcacat cacacagccc tctaaaatg gaaccaaagc 1680
ttcccagctc cctcaaagct ttggatgcaa agaaggcacc ctgacttcca caagacacca 1740
gaattcacac ggtactcaga ggcactgctg gggaagtttg ttggtcttta ttagataaat 1800
ttccagagac ctgtccataa taccacacag aacatgactg tttctttgag gaaagggtta 1860
taatgtctgt ggtgtacaag tcgttttttg tataacttct ttctgtctgc tctgtcttcc 1920
cggcaaacat agttttccta tttcaggcag agtgcggtat attccaggaa acactgtttc 1980
ctactcactt agcttacttc tttgttgaat gcctcactaa tggcaagttt caagatgttt 2040
tgggtgacaa tgcacacatg ctgggcaaaa ggggtgatggc cagtggctgg cagctgggcc 2100

agcagaagct aggacatctg tgagttgtca ttctcatcta tccatgtcca ctggcctgcc 2160
agcatccgcc agtgcttgc cagtgtgcac ggtccacac tgtggccctt gactcccta 2220
atgtacacgc tgcagccaga atgcagatgg agctggcttg gctgttccct ggatgggcaa 2280
taaagaaagt gctgcatccc aaaaaaaaaa aaaaagtaaa aaaaaaagg g 2331

```

(2) INFORMATION ON SEQ ID NO. 5:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1925 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

aataaaaaaa attgtattta cttagaagca ttcagaatgt caacaaaaca gccgcaattt 60
tttttttgca attacagagt ggtattcagt taacagaaca acaattatct tcgtataagc 120
tgcacagag acaactgaag atgaaaaaaa taaaacccaa aaagaaaacc aaaagaaaaa 180
aaaaaaaaaa acaaaaaaca aaactacat ccccatatat aactaatttg tgctgtgcac 240
caacaagaac ctgctttaaa tttccatgcc aatttacaac ccccatactg taccaggcaa 300
ggttagtggc tattgaaaat accaccagga cagggtatc taaagacaca ttcggtagtg 360
tgtaactat acaaaaaaag aactgtaca gtttaaaaaa aaatcttaca cagccttaca 420
tttcaatttt ttctttttaa aggagtgaag tgtgtacagg ggggttaaat gctttataga 480
caagaaaaaa aaaactgcgc tagaaccaac ttattcatca tcatcatctt cttcttcac 540
ttcatcttct tcatcttctc cctcctctc atcctcttca tcttctctc cttcctctc 600
ttccttcttt ttcttgcttt tttcagcctt gacaactccc ttttttgctg catcaggctt 660
tcctttagct cgatatgcag caatatcctt tcgtatttt tccttcaact cgcagccttc 720
ttttcataag gctgcttgct atctgcagca gtgttattcc acatctctcc cagtttcttc 780
gcaacatcac caatggacag gccaggatgt tctcctttga tttttggcgc atactcagag 840
cagaagagga agaaggccga aggaggcctc ttgggtgcat tgggacctt gaacttcttt 900
tttgctccc ctttgggagg gatataggtt ttcatttctc tttcataacg ggccttgctc 960
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gagcacttct tagaaaaact tgagaagttg actgaagcat ctgggtgctt cttcttatgc 1080
tctcccgcac aagtttgac aaaaaatgca tatgatgaca ttttgctctc cggcttctta 1140
ggatctcctt tgcccatggt tagttatttt tctaaaaaat aaaataaata tttgatgtta 1200
gcaataaaat tatgacatat aagaccttaa agtacttagt aagggaatga aaaccaaagt 1260
actggttatt taacacagta gcgacatcaa cctccgtaaa atcagacaag aatatggcgc 1320
agagattaaa ttccctgaag gggctatgcc aagcaaaaca aacaaaaca aaacagtcct 1380
tcaggcgcat ctcaaaaagt ctagacacaa agatataccc atacagtatt ccctatctat 1440
ccgcccagat ctgctctgaa tgagtatcta actggtcact taaacgattt taaaatctag 1500
aacaccattt taaaccaacc aaaccaaagg tcagaaaaa tgctgccaat tcgtggcttt 1560
gcactagata gggaataaac aagggccta gcgagtcgac tcttccta at tatgggacct 1620
taaaaaaaa aatcacogtg caccgaaagt ttcaaaaaa accctctttg cataaaactt 1680
tgctccaaag agggagcagc agccagctcc ggtgctcgga acccggttg gaggtgcggt 1740
gccaccgcga ggcagcctcg ttctctatcg gtttggccct gagatgtatt tctgttctga 1800
ctaaacacgt ccggtctgaa gtttctccga gtaaaacaag atgagggaca aaagccactc 1860
ctgctcgtgg ctcggtggcc cctccccc actcggaag tatttttttg agccgtcaaa 1920
gttg
1925

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(2) INFORMATION ON SEQ ID NO. 6:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1368 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

gtcgggggagc gcgggggccgg ggcccaggggg accccggggcc acggagagcg ggaagaggat 60
ggattgccccg gccctccccc cggatggaa gaaggaggaa gtgatccga aatctgggct 120
aagtgtctggc aagagcgatg tctactactt cagtccaagt ggtaagaagt tcagaagcaa 180
gcctcagttg gcaaggtacc tgggaaatac tgttgatctc agcagttttg acttcagaac 240
tggaagatg atgcctagta aattacagaa gaacaaacag agactgcgaa acgatcctct 300
caatcaaaat aagggtaaac cagacttgaa tacaacattg ccaattagac aaacagcatc 360
aattttcaaa caaccggtaa ccaaagtcac aaatcatcct agtaataaag tgaaatcaga 420
cccacaacga atgaatgaac agccacgtca gcttttctgg gagaagaggc tacaaggact 480
tagtgcacat gatgtaacag aacaaattat aaaaaccatg gaactaccca aagggtcttca 540
aggagttggt ccaggtagca atgatgagac ccttttatct gctgttgcca gtgctttgca 600
cacaagctct gcgccaatca cagggcaagt ctccgctgct gtggaaaaga accctgctgt 660
ttggcttaac acatctcaac cctctgcaa agcttttatt gtcacagatg aagacatcag 720
gaaacaggaa gagcgagtac agcaagtacg caagaaattg gaagaagcac tgatggcaga 780
catcttgctg cgagctgctg atacagaaga gatggatatt gaaatggaca gtggagatga 840
agcctaagaa tatgatcagg taactttcga ccgactttcc ccaagagaaa attcctagaa 900
attgaacaaa aatgtttcca ctggcttttg cctgtaagaa aaaaaatgta cccgagcaca 960
tagagctttt taatagcact aaccaatgcc tttttagatg tatttttgat gtatatatct1020
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tcaagcagga ccctaagatg aagctgagct tttgatgcca ggtgcaatct actggaaatg1140
tagcacttac gtaaaacatt tgtttccccc acagttttta taagaacaga tcaggaattc1200
taaataaatt tcccagttaa agattattgt gacttcactg tatataaaca tatttttata1260
ctttattgaa aggggacacc tgtacattct tccatcatca ctgtaaagac aaataaatga1320
ttatattcac aaaaaaaaaa aaaacaccgg gggggggccc gggcccca 1368

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(2) INFORMATION ON SEQ ID NO. 7:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 424 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

gaatgccctt tggggggccag gggcccctgg gagccccgcc accctttccc acttggccgg 60
ggtgcccgcg gccgccaccc ctgcacgcat ggcaggctgg cccccccca gagccctccc120
cacagccagc agcctttcca cagtcactgc ccttcccgcg gtccccagcc ttccctacgg180
cctcaccgcg accccctcag agcccagggc tgcaacccct cattatccac cacgcacaga240
tggtacagct ggggctgaac aaccacatgt ggaaccagag aggggtcccag gcgcccagg300
acaagacgca ggaggcagaa tgaccgcttg tccttgctg accagctggg gaacaaccct360
ggaccgaggc atcggccagg acccatagag cacccggtt ttccctgtgc ccttttgaa420
attg
424

```

(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

caagtaaattg cagcactagt ggggtgggatt gaggtctatgc cctggtgcat aaatagagac 60
tcagctgtgc tggcacactc agcggctctg gaccgcatcc tagccgccga ctcacacaag 120
gcaggtgggt gaggaaatcc agagttgcca tggagaaaat tccagtgtca gcattcttgc 180
tccttggtggc cctctctac actctggcca gagataccac agtcaaacct ggagccaaaa 240
aggacacaaa ggactctcga cccaaactgc cccagaccct ctccagaggt tggggtgacc 300
aactcatctg gactcagaca tatgaagaag ctctatataa atccaagaca agcaacaaac 360
ccttgatgat tattcatcac ttggatgagt gccacacag tcaagcttta aagaaagtgt 420
ttgctgaaaa taaagaaatc cagaaattgg cagagcagtt tgtcctctctc aatctggttt 480
atgaaacaac tgacaaacac ctttctcctg atggccagta tgtccccagg attatgtttg 540
ttgacccatc tctgacagtt agagccgata tcaactggaag atattcaaac cgtctctatg 600
cttacgaacc tgcagataca gctctgttgc ttgacaacat gaagaaagct ctcaagttgc 660
tgaagactga attgtaaaga aaaaaaatct ccaagccctt ctgtctgtca ggccttgaga 720
cttgaaacca gaagaagtgt gagaagactg gctagtgtgg aagcatagtg aacacactga 780
ttaggttatg gtttaattgtt acaacaacta ttttttaaga aaaacaagtt ttagaaattt 840
ggtttcaagt gtacatgtgt gaaaacaata ttgtatacta ccatagttag ccatgatttt 900
ctaaaaaaaa aaataaatgt tttgggggtg ttctgttttc tccaaaaaaaa aaaaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaattgcc cccaagggga cgggttacaa ttggggggcg1020

```

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 718 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

tgaaaaagta aactacattt cctagcgtgc ccgtgtcttg cttccggctg acgtgtcttt 60
caggaagagg agctggtgag aagacagcga aatggcgctt ccggcccccg gcccggcctc120
cggcggctcc ggggaggtag acgagctgtt cgacgtaaag aacgccttct acatcggcag180
ctaccagcag tgcataaacg aggcgcacgg gtgaagctgt caagcccaga gagagacgtg240
gagagggacg tcttcctgta tagagcgtac ctggcgacga ggaagttcgg tgtggtcctg300
gatgagatca agccctcctc ggccctgag ctccaggcgg tgcgcatgtt tgctgactac360
ctcgcccacg agagtcggag ggacagcatc gtggccgagc tggaccgaga gatgagcagg420
agcgtggacg tgaccaaacac caccttcctg ctcatggcgg cctccatcta tctccacgac480
cagaacccgg atgcggccct gcgtgcgctg caccaggggg acagcctgga gtgcacagcc540
atgacagtgc agatcctgct gaagctggac cgcctggacc tcgcccggaa ggagctgaag600
agaatgcagg acctggacga ggatgccacc ctacccagc tcaaggtctt ggtaagcttg660
caacgggtgt aaaagctcaa ggatccttct gatttcaggg attggtaaaa ttgttcca 718

```

(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

gcaggaccgt cattgacgcc atgagcgcgc tgctgcggt gctgcgcacg ggtgccccag 60
ccgctgcgtg cctgcggttg gggaccagt cagggaccgg gtcgcgccgt gctatggccc 120
tgtaccacac tgaggagcgc ggccagccct gctcgcagaa ttaccgcctc ttctttaaga 180
atgtaactgg tcactacatt tccccctttc atgatattcc tctgaagggt aactcctaaag 240
aggaaaatgg cattcctatg aagaaagcac gaaatgatga atatgagaat ctgtttaata 300
tgattgtaga aatacctcgg tggacaaatg ctaaaatgga gattgccacc aaggagccaa 360
tgaatcccat taaacaatat gtaaaggatg gaaagctacg ctatgtggcg aatatcttcc 420
cttacaaggg ttatatatgg aattatggta ccctccctca gacttgggaa gatccccatg 480
aaaaagataa gagcacgaac tgctttggag ataatgatcc tattgatgtt tgcgaaatag 540
gctcaaagat tctttcttgt ggagaagtta ttcattgtgaa gatccttgga attttggtc 600
ttattgatga aggtgaaaca gattggaaat taattgctat caatgcgaat gatcctgaag 660
cctcaaagtt tcatgatatt gatgatgtta agaagttcaa accgggttac ctggaagcta 720
ctcttaattg gtttagatta tataaggtac cagatggaaa accagaaaac cagtttgctt 780
ttaatggaga attcaaaaac aaggcttttg ctcttgaagt tattaaatcc actcatcaat 840
gttggaagc attgcttatg aagaagtgt atggaggagc tataaattgc acaaactgc 900
agatatctga tagccctttc cgttgcactc aagaggaagc aagatcatta gttgaatcgg 960
tatcatcttc accaaataaa gaaagtaatg aagaagagca agtgtggcac ttccttggca 1020
agtgattgaa acatctgaaa ttctgctgtc aagattccca tctctaagga ctccaagtgc 1080
tagagacaag ggggtctatg agcatttact gacttcctgt taaaacttca ttttttcaaa 1140
ctttttgagc tatgcaatat ataaataaac agtaagaatt ttaaattaaa aaaaaaaaaa 1200
aa

```

(2) INFORMATION ON SEQ ID NO. 11:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1610 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

ggagccggga ctgcggggcg gcgggcgggg gcgtcgctgc ggggctggcc ggtgaggccg 60
cgcatgggg cgagtgcagc tcttcgagat cagcctgagc cacggccgcg tcgtctacag 120
ccccggggag ccgttggctg ggaccgtgcg cgtgcgcctg ggggcaccgc tgccgttccg 180
agccatccgg gtgacctgca taggttcctg cggggtctcc aacaaggcta atgacacagc 240
gtgggtagtg gaggagggtt acttcaacag ttccctgtcg ctggcagaca aggggagcct 300
gcccgctgga gagcacagct tccccttcca gttcctgctt cctgccactg caccacagtc 360
ctttgagggg cctttcgga agatcgtgca ccaggtagg gccgccatcc acacgccacg 420
gttttccaag gatcacaagt gcagcctcgt gttctatata ttgagccctc tgaacctgaa 480
cagcatccca gacattgagc aaccaacgt ggccctctgcc accaagaagt tctcctacaa 540
gctggtgaag acgggcagcg tggctctcac agccagcact gatctccgcg gctatgtggg 600
ggggcaggca ctgcagctgc atgccagctg tgagaaccag tcaggcaagg acaccagccc 660
tgtgtggccc agtctgctgc agaaagtgtc ctataaggcc aagcgctgga tccacgacgt 720
acggaccatt gcggaggtgg aggtgcccgg cgtcaaggcc tggcgggcgg cgcagtggca 780
cgagcagatc ctggtgcctg ccttgcccca gtgcgcctg cggggctgca gcctcatcca 840
catcgactac tacttacagg tctctctgaa ggcgcgggaa gctactgtga ccctcccggg 900
cttcattggc aatattgctg tgaaccatgc ccagtgagc ccccgccag gcctgggggt 960
gcctcctggg gcccacccc tgggtgtgcc ttccgcacca cccaggagg aggtgaggc 1020
tgaggctgcg gctggcggcc cccacttctt ggaccccgctc ttctctcca ccaagagcca 1080
ttegcagcgg cagcccctgc tggccacctt gagttctgtg cctggtgcgc cggagccctg 1140
ccctcaggat ggcagccctg cctcacacc gctgcaccct cccttgtgca tttcaacagg 1200
tgccactgtc ccctactttg cagagggtc cggggggcca gtgcccacta ccagcacctt 1260
gattcttctc ccagagtaca gttcttgggg ctacccctat gagggcccac cgtcttatga 1320
gcagagctgc ggcggcgtgg aaccagcct gacccctgag agctgacccc gtgctgcctt 1380
ctccaggcag gccgggctgc tgcctggga ctggggcgcc cagggcctcg tgccttctct 1440
cttggcctag cctggccac tcaggacctg ccagcctct gccagctcct ctgcatccgc 1500
cctcttctcc ctggggctgg ggtgggggtg gcaggagct gggacctgga gagacaactc 1560
ctgtaaataa aacactttat ttgtagaaaa aaaaaaaaaa aaaaaaaaaa 1610

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(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2155 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

cacgcaagga  tgaggcgggg  ttctgcgctg  gcgcgcgatgc  gtgcagcaaa  gaattggagga  60
gtcggaaacc  gaacggaagc  gggctcgcac  cgacgaggtg  cctgccggag  gaagccgctc  120
cgaggcgga  gatgaggacg  acgaggacta  cgtgccctat  gtgccgttac  ggcagcgccg  180
gcagctaactg  ctccagaagc  tgctgcagcg  aagacgcaag  ggagctgcgg  aggaagagca  240
gcaggacagc  ggtagtgaac  cccggggaga  tgaggacgac  atcccgtag  gccctcagtc  300
caacgtcagc  ctccctggatc  agcaccagca  ccttaaagag  aaggctgaag  cgcgcaaaaga  360
gtctgccaa  gagaagcagc  tgaaggaaga  agagaagatc  ctggagagt  ttgccgagg  420
ccgagcattg  atgtcagtga  aggagatggc  taagggcatt  acgtatgat  accccatcaa  480
aaccagctgg  actccacccc  gttatgttct  gagcatgtct  gaagagcgac  atgagcgct  540
gcggaagaaa  taccacatcc  tgggtggagg  agacggatc  ccaccacca  tcaagagctt  600
caaggaaatg  aagtttctct  cagccatcct  gagaggcctg  aagaagaaag  gcattcacca  660
cccaacaccc  attcagatcc  agggcatccc  caccattcta  tctggccgtg  acatgatagg  720
catcgctttc  acgggttcag  gcaagacact  ggtgttcacg  ttgcccgta  tcatgttctg  780
cctggaacaa  gagaagaggt  tacccttctc  aaagcgcgag  gggccctatg  gactcatcat  840
ctgccctctg  cgggagctgg  cccggcagac  ccatggcatc  ctggagtact  actgccgct  900
gctgcaggag  gacagctcac  cactcctgcg  ctgcgcctc  tgcattggg  gcatgtccgt  960
gaaagagcag  atggagacca  tccgacacgg  tgtacacatg  atggtggcca  cccggggcg  1020
cctcatggat  ttgctgcaga  agaagatgg  cagcctagac  atctgtcgt  acctggccct  1080
ggacgaggct  gaccgcatga  tcgacatgg  cttcgagggt  gacatccgt  ccatcttctc  1140
ctacttcaag  ggccagcgac  agaccctgct  cttcagtgcc  accatgccga  agaagattca  1200
gaactttgct  aagagtggcc  ttgtaaagcc  tgtgaccatc  aatgtgggc  gcgctggggc  1260
tgccagcctg  gatgtcatcc  aggaggtaga  atatgtgaag  gaggaggcca  agatggtgt  1320
cctgctcgag  tgctgcaga  agacacccc  gctgtactc  atctttgcag  agaagaaggc  1380
agacgtggac  gccatccacg  agtacctgct  gctcaaggg  gttgaggccg  tagccatcca  1440
tgggggcaaa  gaccaggagg  aacggactaa  ggccatcgag  gcattccgg  agggcaagaa  1500
ggatgtccta  gtageccacg  acgttgctc  caagggcctg  gacttccctg  ccatccagca  1560
cgtcatcaat  tatgacatgc  cagaggagat  tgagaactat  gtacaccgga  ttggcgcgac  1620
cgggcgctcg  ggaaacacag  gcatcgccac  taccttcac  aacaaagcgt  gtgatgagtc  1680
agtgtgatg  gacctcaaag  cgctgctgct  agaagccaag  cagaagggtg  cgccgtgct  1740
gcagggtgct  cattgcgggg  atgagtccat  gctggacatt  ggaggagagc  gcggctgtgc  1800
cttctgoggg  ggctgggtc  atcggatcac  tgactgccc  aaactcgagg  ctatgcagac  1860
caagcaggct  agcaacatcg  gtcgcaagga  ctacctggcc  cacagctcca  tggacttctg  1920
agccgacagt  cttcccttct  ctccaagagg  cctcagtc  caagactgcc  accagtctac  1980
acatacagca  gccccctgga  cagaatcagc  atttcagctc  agctggcctg  gaatgggcca  2040
ggctggctct  ggctgcctgt  tccctgtgct  cttcagaatt  actgtttttg  tttcctttta  2100
ccccagctgc  cattaaagcc  caaacctcta  gcccaaaaaa  aaaaaaaaaa  aaaaaa  2155

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(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1743 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

cctgggcggg ccctgcgtca ggttgagtt tcacttttag ctctgggcac ctccagctcc 60
tgctcgccgg acggctccca gggagagcag acgcgccaga cgcgccaccc tcggggcgcc 120
gacggtcacg gagcatgggg tcggcctttg agcgggtagt ccggagagtg gtccaggagc 180
tggaccatgg tggggagttc atccctgtga ccagcctgca gagctccact ggcttccagc 240
cctactgcct ggtgggttag aagccctcaa gctcatggtt ctggaaaccc cgttataagt 300
gtgtcaacct gtctatcaag gacatcctgg agccggatgc cgcggaacca gacgtgcagc 360
gtggcaggag cttccacttc tacgatgcca tggatgggca gatacagggc agcgtggagc 420
tggcagcccc aggacaggca aagatgcagc gcggggccgc ggtgtctgac agctccagca 480
cctcaatgaa tgtgtactcg ctgagtgtgg accctaacac ctggcagact ctgctccatg 540
agaggcacct gcggcagcca gaacacaaag tcctgcagca gctgcgcagc gcggggacaa 600
cgtgtacgtg gtgactgagg tgctgcagac acagaaggag gtggaagtca cgcgcacca 660
caagcgggag ggctcgggcc ggttttccct gcccgagacc acgtgcttgc agggtagagg 720
ccagggccat ctgagccaga agaagacggg caccatcccc tcaggcagca ccctcgcat 780
ccgggtggcc cagctggtta ttgactctga cttggacgtc cttctcttcc cggataagaa 840
gcagaggacc ttccagccac ccgcgacagg ccacaagcgt tccacgagcg aaggcgctg 900
gccacagctg ccctctggcc tctccatgat gaggtgcctc cacaacttcc tgacagatgg 960
ggtccctgcg gagggggcgt tcactgaaga cttccagggc ctacgggcag aggtggagac 1020
catctccaag gaactggagc ttttgacag agagctgtgc cagctgctgc tggagggcct 1080
ggagggggtg ctgcgggacc agctggccct gcgagccttg gaggaggcgc tggagcaggg 1140
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ccggcctggg tcttgctgga cgagtgtggc ctagagctgg gggaggacac tccccacgtg 1500
tgctgggagc cgcaggccca gggccgcatg tgtgactct acgcctccct ggcactgcta 1560
tcaggactga gccaggagcc cactagcct gtgcccgggc atggcctggc agctctccag 1620
cagggcagag tgtttgccca ccagctgcta gccctaggaa ggccaggagc ccagtagcca 1680
tgtggccagt ctaccatggg gcccaggagt tggggaaaca caataaaggg ggcatacga 1740
gga

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(2) INFORMATION ON SEQ ID NO. 14:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 970 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

cggtctgagt gggtttttag tttgttcctt ctttttgaag tcccttcatt tcaatccttg 60
actctctctc cccttcctt gccagctct gttgaatgct gctgtgcgcg tgtgagggcc120
gctctgcaca cagggccctt gggttgtgtg aactgaaatt ctccctgtat ttgtgagact180
cgcaggagtc cccatctgta gcacaggcaa tgccagtgcc atgctgcagc ctcagaaaacc240
aggcctctca ctccagcagc aggcagaacc gtgtctgtgg tcgggtgctg tccacagctc300
tgtctgcctt gttcttgggc ttgagctgga tagaggtggg gtctcttcac cttccctgaa360
ttcagaacag accctgtgcc tggcccagc gtgcccaggc aattccccag gccctcattg420
ggagcccttg gtgttctgag cagcagggcc caggcagcac atgagcagtg cccaggggct480
ccctgcgtga ggacggcaag gtgcgatgta tgtctaactt attgatggca ggcagcccc540
tgtgccccct aagcctggcc ctggttattg ctgagctctg tgctcagtgc tgcggcctgg600
ccgtggctcg tctgttcctt tggggggccc gggcgggttg tgggaatcag tcttcacaga660
cagacgtgag ccaggcggag gactcgttcc ttgcagaggt cagtcctcac ctgcagggtg720
cgggggtggg gggggcaagg aggggcaggc acacaccatg tctgacctga acccgattct780
ggggagcatc ttcccgctcc ggcccacga cctccacagg gttacattgt aatatatatg840
ccccagctaa cctgtctgat ggtggcatct tcctgcagac atttcaaaca tgtaactttt900
atatgaaaaa aaataaacac agatgaaagc tgcccaatgc caaaaaaaaaa aaaaaaaaaa960
aaaaaaaaaa

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970

(2) INFORMATION ON SEQ ID NO. 15:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2003 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

gagagatctg aaataacctt tcccagtggg caggggtgccc aggggttgagg ggacagcaca 60
taccaccccc acccaacctg ttcgaggggc cctgcatggc acgggatgag tccctgccct 120
gtgcagctgc ctggcagtggt ctgggacaag gatcttgtag ccagcacaga ggcctcttca 180
aaggcctctc cctcttggtg ctccaggcaa ggcaggtgccc cgcttccccca acacctccag 240
gcagtgaccc tagggcatgc cccagcaggt ctccgagcag ccactgggac ccgtctcagc 300
acatcctggc ctttgaaagt ctgatatcct gagaggaggg caggttttag ggccgcagtt 360
ccagccagcg tccccagcct ggcttcctgt ccatggactc agtagctcgt ggggcttctt 420
accacccacc agccccgtg ggggtgcggc tggctgtggg caaaggagga cttgcctgga 480
gatttgagag aagattcctt ctaccagggc tgctgagggg ccaggcctgc atcaggggct 540
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atgctgcctc agacaaaggc agtgagcctt ccctgccaaa gtgcccattc catgggctcg 660
gcctcactgg tcaactgttag cccatgaaca cgtgtggggc tcggtcacgt ggctttgagg 720
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tctaattgtc ccacatgtag cctggcagtc caaagaccaa gaatcaactt gcaaactctc 840
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cagccaccca ggtgccattt ccagtctgac ttccagaaat gtgcaccatg tcctagagca 1140
cagacccatt ggctggagcc tcctgggagg gttcaaacca tcagctctat gagaaatgcc 1200
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agccacagg gtcaagtcaat gtatcttcta cgtgcctctc cctctgcctt ctctcacagt 1620
gcccccggt ccagagctca ggggtagggg ttctcctgag ggtgcagggg atccttctca 1680
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ctggacccct gccaggtctg tggacatggt tatatgccc ggagaggggg gtgcagggcc 1860
ccagggatgg cccccaatcc cacctctgtt tattctgtaa actgcaacct ataaataacc 1920
tttagcattc ctattgtaac aaaattaatt tttatgaaat aaatttatatt tctagtctat 1980
ataaaaaaaaa aaaaaaaaaa aaa
2003

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(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2279 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

gattgaatta agcccttggg tttgccccac tgcagcttca agcggaaagg aaggaaccag 60
ttggaccagt ggtcacagac ccaagcaaaa ggcgaccgca atcagcagct gggctcacc 120
cctttcctct gaaccagtga cccaacacct tcaccctcga ttgggcaacc ttggcctggg 180
gcatgtttat caccactgaa gtgacttgca gctatcaaag accagttaga ggggtgtgcag 240
caagcacttt ctcaggctgc ccccatccca gaagaggaca cagacactga agaaggtgat 300
gactttgaac tacttgacca gtcagagctg gatcaaattg agagtgaatt gggacttaca 360
caagaccagg aagcagaagc acagcaaaat aagaagtctt caggtttcct ttcaaactctg 420
ctgggaggcc attaatctag gaatcagctt gcaacagagc acaaaaaaca ccaaaaaaat 480
ttcaaacaaa aaaaaaaaaa aaaaaaggaa aagaaaaaaa ttgaactgta agctttaatg 540
attactttag atttgtttta ttttcctcc tgcagtgaat taattggata tatatcagct 600
gacactgata gattgatatt tctgatcgtt atttttgtgt aataagcatg gaaatgaact 660
ttatacacac cactgtgttg tcagagataa atattagggg ttgtttttaa agcaaaaaga 720
aaaaaacaaa aaccaaacta ttaaaatcct cctataaata ttctttttct ttacagtttt 780
tcaagcatgc aaaacagttt attgtaactt actgaaaaat attacaatt aattgtgaat 840
acatgctgtt accagcttcc ttattcctaa tacctggaaa attttttttt caacggatag 900
atthttgatgt aaaaaagacc gaaattatca aggtatctta gttgaaggac ttgggaaata 960
ctatcaaaat taatttctta ggaaaaaatt taaaagtata ttttaagtact ctggatagac 1020
tgaaacgttt ccatgttatt tctgcagttg tagacttagg cttatttgta aagaagcatg 1080
ctccattgac tgccatctct agtcttgcat tgggtggtat taacccatag aaagcaagca 1140
gttgtgtatc acatagacaa tgggttatgat gtaaacagat tcagttgttt tgttgttcat 1200
tcgtcatatg tttgtgatag ggatgttggg agcacagctc tattctgcct gctcagactt 1260
aagtttagac cttatctttt atattatgtc atgaaaaaag tctcctaaaa ttgtgaaact 1320
agttcttgat gagtgatgtg atcatcagca ataaagatat aataactctg ttttcttagc 1380
ctgtatagag gagaggaact tgcttggtt taaaatatat ttatttgcca ttttaagtata 1440
aatatgaaat ctgtttctta ttgggaagat agaatatata tattttcctt taaacttttt 1500
aaggtcactt ttaaataacc aaatttgatt tatggttttt aacaaaggac taaagagctg 1560
aaaccaacct agttttgttt ttgtgatata aactttaagt gtcgagggac catgccagca 1620
actacaaaaa atctcttaaa tcttcaggta cagctggcat tttggcagat gcatagagac 1680
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tttctattta tcccttatat ttctaaagac taattataag taatctgaca ttttaagtata 1800
gctactctta tttatttttt ctttctgagg tattaaaata tctggactga gttttgcca 1860
atgttaaagg gagaagagtt actgaagact ttgaacactt gctttttgtg attgcttatg 1920
tcattagtgc ctcatgactg tgtttgatgt cctttattga tacaaagtga gcctgtgcct 1980
tcattatctt gccattttta atacaaatgg aaacctgggt tttgaaaatc tctgaactgt 2040
gtgggttttg gaggaatata cctgaatttt attcaataac agtttctgga caggaagaaa 2100
aatacagtta catatttata aaatagtcgt tatcagtatt tttttatgtg tatgtttctt 2160
tctttaaaac aatattcttg gatataaagt agaaaagttt aaaggtcatt tccatttctt 2220
cactaaggag aaaaaaagtt aaataatcca agtaattaaa gatataagtc actagatga 2279

```

(2) INFORMATION ON SEQ ID NO. 17:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 761 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

aaatcttagg gtaagccagc tgccttggaa gccaccagc gctccagact gcagggaaga 60
agccgggagc aggcagccat acctccactc ttgtcctcaa ggactcagct gtgtggcctt120
ggatttcttt ttgcgggact tgcgccttgc aggacactgg tgttgagatt ggagggtcct180
atcctgcccc ggggtgactc ccagggttgc agggggatag ggtggagaag ggtgctgtag240
cccttgcaag cgtgaagtcc tttctgctct cttagcctat tacattagga gtagcttacc300
tttgggtgcc aacgggtccag gatcccccta aaatgggatg gggataattc aggaatcagc360
ctgggttggc acaggggagg tattccttgg agaggcagga ctcacacaca cccatccaga420
tcagtgtagc ttctccctta ggaagcctct aggacatccc ccatgttaga gtccacatca480
gcaaagctgc tctgcccttg gctactttca cttgggttac ctgccttggg ctacttccac540
tagctgcaac cctgggacgc atgggagggg aggggtgtga ccctcaggaa cagtgtggtc600
cttggagggt ctagacagac cctgagcatc accacccagc ttattgtgac cccacgtttc660
caccatcagc cctcctgggg tctctgcttg tgtgaacagt agggccaac ctggaaccag720
atggtacggc catgccgggc ctgcaggagg ctcatgctg g

```

(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1403 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

ggtggctttg cctgggtgct gggcctgogt tctctggctg cttgctgcct gtgtgcgttc 60
cttgggtggct ttggcttctg cactccttgg tcttcaccgc tcaggtcctc cattcacacg 120
aggtcctcct cgctctggcc gctcttgctg ctcctgtctg aagaaatcag actgatttcc 180
tcttaagact cctagggatg tggggaagag ctgggactca agtgagctcc acgggtgtgaa 240
acatgagggg ggtgaggtgt ccgtccactt cccccataaa ggtgtgcatt tcagttaggc 300
tgccccgcca cagagcaggc ttcactctgt ctgccatcca gcccatctg gatgtgaggt 360
ggggtggaga catcatgggg tgattgcaga aagggggagt ggcgggccac gcagcttctg 420
ctgaggagct gaccgctctg agctgttctg tttcgtattg ctgctctgtg tctgcatgta 480
ttgtgaccgt gcggtccac ctcttccagc tgetgctaca gctgaggcct ggatccccgc 540
ctttccctgt gacttacgtg tctgtcaccg gcaggcagcc ctacaaatcc tggtgacctg 600
ctctcccaag aacagagcct gtcccagat gtcccagtag cgatgagtaa cagaggtggc 660
tgtggacttc ctctacttct ccttgctgga tcagggcctt cctgcctccc gctgggcagg 720

tctggccttg ctctcttggc agggccccag cccctctgac cactctgcag ctccacctgc 780
agctgatgcc aaagtgtgtg tgtccagtgt gcagcagccc tgggagccac tgccaccttc 840
agaggggttc cttgctgaga ccacattgc ttcacctggc cccacctggt ctgcttgctc 900
ggcccaacct agcgttctgt gccatgctag agcttgagct gttgctcttc ttcaggggag 960
gaaatagggg ggagagcggg aagggctctg ctctaagtg ttgctgctgt ggcttttttg 1020
ccttctccaa agacgcactg ccagggtcca agcttcagac tgctgtgctt agtaagcaag 1080
tgagaagcct ggggtttgga gccacctac tctctggcag catcagcatc ctactcctgg 1140
caacatcagg ccaacgtcca cccagcctc acattgccag atgttggcag aagggtctaat 1200
attgaccgtc ttgactggct ggagccttca aagccactgg gatgtcctcc aggcacctgg 1260
gtcccatgac cagctccccg tctccatagg ggtaggcatt tcaactggtt atgaagctcg 1320
agtttcatta aatatgttaa gaatcaaaac tgtctttgtt caggctgcta taacaaaaat 1380
ataatagcct gggtggctta aac

```

(2) INFORMATION ON SEQ ID NO. 19:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1702 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

gggccgcacc ggagtgtcgg tggatgatggg catcccgagc gtgcggcgcg aggtgcactc 60
gtacctgact gacactctgc actcgctcat ctccgagctg agcccgagg agaaggagga 120
ctcggtcacg gtggtgctga tgcggagac tgactcacag tacacttcgg cagtgcacaga 180
gaacatcaag gccttggtcc ccacggagat ccattctggg ctccctggagg tcatctcacc 240
ctccccccac ttctaccctg acttctcccg cctccgagag tcctttgggg accccaagga 300
gagagtcagg tggaggacca aacagaacct cgattactgc ttctcatga tgtacgcgca 360
gtccaaaggc atctactacg tgcagctgga ggtgacatc gtggccaagc ccaactacct 420
gagcaccatg aagaactttg cactgcagca gccttcagag gactggatga tcctggagtt 480
ctcccagctg ggcttcattg gtaagatggt caagtgcgtg gacctgagcc tgattgtaga 540
gttcattctc atgttctacc gggacaagcc catcgactgg ctcttgagcc atattctgtg 600
ggtgaaagtc tgcaaccccg agaaggatgc gaagactgtg accggcagaa agccaacctg 660
cggatccgct tcaaaccgtc cctcttccag cacgtgggca ctactcctc gctggctggc 720
aagatccaga aactgaagga caaagacttt ggaaagcagg cgctgcggaa ggagcatgtg 780
aaccgcgagc cagagggtgag caccgagcctg aagacatacc agcacttcac cctggagaaa 840
gcctacctgc gcgaggactt cttctgggcc ttccccctg ccgcggggga cttcatccgc 900
ttccgcttct tccaacctct aagactggag cggttcttct tccgcagtgg gaacatcgag 960
caccgcgagg acaagctctt caacacgtct gtggagggtg tgcccttcga caacctcag1020
tcagacaagg aggcctgca ggaggccgc accgccacc tccggtatcc tcggagcccc1080
gacggctacc tccagatcgg ctcttcttac aagggagtg cagagggaga ggtggaccca1140
gccttcggcc ctctggaagc actgcgcctc tcgatccaga cggactcccc tgtgtgggtg1200

attctgagcg agatcttctt gaaaaaggcc gactaagctg cgggtctctg agggtagcct1260
gtggccagcc ctgaagccca catttctggg ggtgtcgtca ctgccgtccc cggagggccal320
gatacgcccc cgcccaaagg gttctgcctg gcgtcgggct tgggcccggc tgggggtccgc1380
cgctggcccc gaggccttag gagctggtgc tgcccccgcc cgccggggccg cggaggaggc1440
aggcgggccc cacactgtgc ctgaggcccc gaaccgttcg caccgcgctt gccccagtca1500
ggccgtttta gaagagcttt tacttgggog cccgcgctct ctggcgcgaa cactggaatg1560
catatactac tttatgtgct gtgtttttta ttcttgata catttgattt tttcacgtaa1620
gtccacatat acttctataa gagcgtgact tgtaataaag ggttaatgaa gaaaaaaaaa1680
aaaaaaaaaa aaaaaaaaaa aa

```

(2) INFORMATION ON SEQ ID NO. 20:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 802 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

tttttttttt ttttttttca ttttcaaaag ggctttttatt aaattctccc cacacgatgg 60
ctcctgcaat ctgccacagc tctggggcgt gtctgttagg gaaaggccct gttttccctg120
aggcggggct gggcttgctc atgggtccgc ggactggccg tgcttgccgc cctggcgtgt180
gtctagctgc ttcttgccgg gcacagagct gcggggctctg ggggcaccgg gagctaagag240
caggctctgg tgcaggggtg gaggcctgtc tcttaaccga caccctgagg tgctcctgag300
atgctgggtc caccctgagt ggcaagggga gcagctgtgg ccggtgctcc ttcctaggcc360
agtcctgggg aaactaagct cgggcccttc tttgcaaaga ccgaggatgg ggtgggtgtg420
ggggactcat ggggaatggc ctgaggagct acgtgtgaag agggcgccgg tttgttggt480
gcagcgccct ggagcgccct tctcctgagc ctcagtttcc ctttccgtct aatgaagaac540
atgccgtctc ggtgtctcag ggctattagg acttgccctc aggaagtggc cttggacgag600
cgtcatgtta ttttcacaac tgtcctgcga cgttggcctg ggcacgtcat ggaatggccc660
atgtccctct gctgcgtgga cgtgcgggtc gggagtgcgc agccagaggc ggggccagac720
gtgcgcctgg gggtgagggg aggcgccccg ggagggcctc acaggaagtt gggctcccgc780
accaccaggc agggcgggct cc                                     802

```

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1647 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

acccttctc tttcttttc cctttttctt tttctttttt gggtaagggt gacaccccat 60
ttattggaga agaccccagc acccgccccc tgaggcttta agggctttgg tgtatccttg 120
gtcacgagcg ctggggccagg aagcagagtt cctgagagcc aagtctagtg gttgagagag 180
gaccctggct gggcctgggg agcaggaagc catctgtcca gctgggcagc ccccatgggt 240
ccctggtgca gccccggcca tgtgtccagc gccccatact ccatgagggg ggtctgcacc 300
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ttctgttggg ctcttgctcc cagcatggat gaccagcga tagcagtcag tgatgcgctt 420
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cagccacagg gccaaacttg gactggggcc atcttccctt gggatttggg gggctttgga 660
atggggatgt gtagggctga tgggtgaggt ctggttagtg gggctctgag agggcaggag 720
gggtggggagg gctgcgggct ggggtggcagc aggcacagag atttgatggg caggagacac 780
aggggacctg gaggtggtgg tcagagaggg ctgggcagtt gggataatgg gaagctgggt 840
ggcctgggtt ctgaggacaa gggcatctgg ggcttgaggg ggtcgctggg caccgagggg 900
ggtgaccaga ggggcatggt taggtgggat tccaggcaaa tgagtgggtg tctgggtgcc 960
agcgaccogg gtgtctggaa acatggggga ctggtgggca gggaagagct ccgcatattt 1020
ggttgagatc atagggggct ggtgggcagg aggtctgtgt gaatgagaga cagagagaat 1080
accgggttg taggcagaag gcagatctgg atagttggct gcgatcacgg ggatctggtg 1140
gtcacgggac aaagctgggt gtgtggcagg gatcacagga ggctggtggg cagaaggcag 1200
tgtgggatgc gtggcagaga ccaccacagg ccgggtgacg gagagcactg aggagtggta 1260
ggggaccctg ggggcaactga gcgggggtgg ccagggtggc tccgggtagg gtatctgtgg 1320
ctctctgtcc tctgggaagc tcggtctata ggccagggca aagtcaggcg gctgcgtagg 1380
ctccatccac aggatcccg gcctctccgt ccagccaccg ttgaagcctt ccaggcctcg 1440
tcttcatctt cctcatctc cccgtcatcc agcaactcat ctccgaggtc ctgggaaccc 1500
tgggcaccca tggcccctgc agggctgcag ctgatgccat cagcctccag ctcatgtccc 1560
tcgctacaat aacactcgaa gccaccaacg tagttgacac acatctgctg gcacacaccg 1620
gcaatctggc actcatctgt gtccaca

```

1647

(2) INFORMATION ON SEQ ID NO. 22:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1170 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

cctcgctggc agaagagata gaatcagggc tgccccaca gagtgggacc caaggggcta 60
attggaggca cgagggggacc cctccccagg gccttttccct cctctgcgtc ttccatctac 120
tgaaatggga gaggggggtgg ggagcttctg ttctggtgaa gggacccggg caggcccca 180
gcaccccatg ctgacttggg gaaccccaaga tctctggggc ccagccaggc aggtgtgtgg 240
ggcagctgtg ccaatctacc tcacaggccc acccctgcc gggcatgccg tgggatcatg 300
ggcaggggaag gctctggggg tcggagacac cgctgcttag cacccccagc cagaacaccc 360
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aaggagacga gcgcttcgcc ttgattctcc gagaagcctc cgagaagtgc tttaatgtgt 480
tttgcatgcg ccaggcgggtg ggcagcgggg gcctgtccag ccctctcccg ccctccttcc 540
ccaagtgaag tccactgctt tgtcaccagc gacctgcctg tcatgcccac cccctgagga 600
agcatgggga ccctaacacc ctggtgcoct gcaccagaca ggccgtggtc aggccaggc 660
caccggccgg gttctgccac agcttcccac gtgcttgctg acatgcgtgt gcctgtgtgt 720
ggtgtctgtt gctgtgtcgt gaaactgtga ccactactca gtccaaacaa gtgagtggcc 780
ctcgaggcca cagttatgca actttcagtg tgtgtcataa cgacgtcact gctttttaa 840
ctcgataact ctttatttta gtaaatgcc caggagtcct ggaagctacg cggacttgca 900
gaggttttat tttttggcct tagaatctgc agaaattagg aggcaccgag cccagcgag 960
cagcctcgga cccggattgc gtttgacctt gcggatatgt ttatacagat gaatataaaa1020
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cgacccacc ccccaaaaaa gctacttctt cattccgtgg tacgattatt tttttaact1140
aaaggaagat aaaattctat attcttaaaa 1170

```

(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1259 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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ggagtatcca gataggcgac acgccggcgg gcggctgagg cggaatggc tgctgtactg 60
cagcgcgtcg agcggctgtc caatcgagtc gtgcgtgtgt tgggctgtaa cccgggtccc 120
atgaccctcc aaggcaccaa cacctaccta gtggggaccg gcccaggag aatcctcatt 180
gacactggag aaccagcaat tccagaatac atcagctgtt taaagcaggc tctaactgaa 240
ttaacacag caatccagga aattgtagt actcactggc accgagatca ttctggaggc 300
ataggagata tttgtaaaag catcaataat gacactacct attgcattaa aaaactocca 360
cggaatcctc agagagaaga aattatagga aatggagagc aacaatatgt ttatctgaaa 420
gatggagatg tgattaagac tgagggagcc actctaagag ttctatatac ccctggccac 480
actgatgatc acatggctct actcttagaa gaggaatatg ctatcttttc tggagattgc 540
atcctagggg aaggaacaac ggtatattgaa gacctctatg attatatgaa ctctttaaaa 600
gagttattga aaatcaaagc tgatattata tatccaggac atggcccagt aattcataat 660
gctgaagcta aaattcaaca atacatttct cacagaaata ttcgagagca gcaaattctt 720
acattatttc gtgagaactt tgagaaatca ttacagtaa tggagcttgt aaaaattatt 780
tacaagaata ctctgagaa tttacatgaa atggctaaac ataactctctt acttcatttg 840
aaaaaactag aaaaagaagg aaaaatattt agcaacacag atcctgacaa gaaatggaaa 900
gctcatcttt agtttcagat taaagaaagc tttgttttat tttgctttga gagaatggta 960
tgttttctta actataggtt attttataga gaataaaaa gtataaaaca ttaaaaataa1020
ccctagatat actttaaaat aatgttatat ttatgctaaa atatgtaaat tacactatac1080
aaccatatga taggttattt ctctaacctt gtcttctaac gttttaccaa aaattcataa1140
tctaatagtt tatcagtttt caatagatta aataaaatga ttactttaaa aataataaaa1200
tttatctaata ttaaagttga aaaaattttt ggccgttagt tatctattac tagtgatca 1259

```

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

gcgttccctcc tccggccctc ggtcaccgcc agcacgcgcc tgcttcccgt ctgcgcgagt 60
ccacgcagct cccagggccc ttcaccagca cagcagcagc aggcattggca gcaagcgtgg 120
agcagcgcga gggcaccatc caggtgcagg gccagggcct cttcttccga gaggccctgc 180
ccggcagtggt gcaggctcgc ttctctgtac tgctgctgca tggatttcgc ttctcctccg 240
agacctggca gaacctgggt aactgcaca ggctggccca ggctggctac cgggctgtgg 300
ccattgacct gccaggtctg gggcactcca aggaagcagc agcccctgcc cctattgggg 360
agctggcccc tggcagcttc ctggcggctg tggtgatgc cttggagctg ggcccccg 420
ttgtgatcag tccatcactg agtggcatgt actcctgcc cttcctcacg gcccctggct 480
cccagctccc gggctttgtg ccagtggccc ccattctgac tgacaaaatc aatgctgcca 540
actatgccag tgtgaagact ccagctctga ttgtatatgg agaccaggac cccatgggtc 600
agaccagctt tgagcacctg aagcagctgc ccaaccaccg ggtgctgatc atgaaggggg 660
cggggcaccg ctgttacctg gacaaaccag aggagtggca tacagggtg ctggacttcc 720
tgcaggggct ccagtgaagc ccagcactgc tgcagggggt gggctgcctg cctgctctga 780
gctctctctt gcacgctctc tcttctctcc caggctctgg ctcatgcaca tgcaacaggt 840
gcgtctgtct atatgtctgg gttcttgtct tttgtggtct gtttgccttt tctacctctt 900
tctcttgtag tgatagactg agggggtaaa atcaagagga aaaaactctc aggaatcaag 960
gaacataatc ctgtggagggt taaaccatta catgaggctt ctcccgggtc gttcaagttt 1020
c

```

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1407 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

agcaaagggtt gccggagacc aagatcggaa gcgtgaaata cgaaggcatc gagttcattt 60
aactgaaaac cggctcaagg agcaaggcca tcaggactca gcttttataa aaacaagagg 120
agtgcacttt tgttttgttt tgttcttttt ggaactgtgc ctgggttgga ggtctggaca 180
gggagcccag tcccgggccc catagtgggt cgggcactgg acccccgggc cccacggagg 240
ccgcggctct aactgctttc catgctgcca tctgggtgtg atttcgggtc cttcaggcat 300
tgactcaagg cctgcctaac tggctgggtc gtttcttcca tccgacctcg tttcttttct 360
ttcctatgtt cttttgttca gtgaatatcc cttagagctcc taccatatgt caggccctat 420
gcctcaccct gagaacgcag tgggcatgag gtggacctgt ttgctgggaa ccccagggtc 480
cccccttttc ttcctactct gtgcctggag catcatgtcc acccctgcag atccttggaa 540
aagaaaatgt ttatgttgca gggatttgca tggtcacgag tgagggcagg cccctgggga 600
cacatctgcc cacagctgca caggccaggg cgcaggcaca tctgttggtt ctcaggcctc 660
agataaaacc atctccgcat catatggcca gtgaccgctt tctcccttca agaaaattct 720
gtggtctgtc agtactttga agttttaatt attaacctgc tttaattaaa gcagtttctt 780
ttcttataaa gtggaatcac caaatcttat cacacagagc acagtcctgt agttaccag 840
cccgtccag cagtgcggga gattgtaagg aagcgggtgg ggctggtgaa gcaagtctca 900
catgtcggcg ttcttgccca atggatacaa agataaagaa aatgttgctt ttttctagga 960
actgtcagaa atcctcatgc ctttcaagac ttctgtgaat gacttgaatt ttttattccc 1020
tgccatagggt ctgtgaacga ggccgtgtct ttccttggg tttctttcca tggcctttat 1080
ttctctctct ccagtgggag ttttgaggc tcttctctgt ggaaacttca cgagcggttg 1140
ctgggcctcg gcttcgctgg agtgactcc agggagaagg cagagtggga tttgagaccc 1200
aggttaggca cgaccaggc tgagaaggga cgtttccatc attcacagt cccctccca 1260
agcactacct cagcccgagc cccaccctca ctccacccc acccccgcat cgtcaggggt 1320
gccacgggtg gccggagggt gcccgcctcg ggcttgttcc tgttgccggt ccctgaaaaa 1380
gcttttcccc ttttgaaatt caagcac

```

(2) INFORMATION ON SEQ ID NO. 26:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 286 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

ctctcggctc cgcttggcag cagctccgcc gccagaggc gtccgagacc ctccgactcg 60
tgggtacgca taggcctcgc cagcgagcct tgcccaggca acgagtcgcc agcccgcccc120
ctcgccgagg gctaggtctc acctcgccac cagtacgtct tggacaagta gtgccagggtc180
tgatgccggg tgtggtgagt gccgcccggg cccagggtgcg ccgcctcgat gaggtcccgg240
cgtcgctccg gctgcagcac cacctccagc tccgcgaagg tcttgc 286

```

(2) INFORMATION ON SEQ ID NO. 27:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 815 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

cgccctcgttt gcaactgggtg ctggacagcc gacgcaacta caaatggggc ggagtttcgg 60
cactggagca gctaatttgc atataggaat gagtcccccac aaacacgaga agttccagca120
agttcgccac ttccggttct cctggctatc caatagcatc gaggaggagca tccccggaag180
tgaggcagcg gaggacgacc tttttccggt tccggcctgg cgagagtttg tgcggcgaca240
tgaaactgct taccacaat ctgctgagct cgcagtgtgc ggggggtggg tcccgtggct300
tccccctgcg cctccaggcc accgaggtcc gtatctgccc tgtggaattc aacccaact360
tcgtggcgcg tatgatacct aaagtggagt ggtcggcggt cctggaggcg gccgataact420
tgctctgat ccagggtgcc aaagggccgg ttgagggata tgaggagaat gaggagtttc480
tgaggaccat gcaccacctg ctgctggagg tgaagtgtat agagggcacc ctgcagtgcc540
cggaatctgg acgtatgttc cccatcagcc gcgggatccc caacatgctg ctgagtgaag600
aggaaactga gaggttgattg tgccaggcgc cagtttttct tgttatgact gtgtattttt660
gttgatctat accctgtttc cgaattctgc cgtgtgtatc cccaaccctt gacccaatga720
caccaaacac agtgtttttg agctcggtat tatatatatt tttctcatta aaggttttaa780
accaaaaaaa aaaaaaaaaa aaaaaaaagt cgacg 815

```

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

tttctcgaac cttctctttt ctttcttttt tgcactgtgc aaatatattg actttatttg 60
tctcctttca ggagcctcac agacatatcc aggtaaaaag atcgttaaat aaatgccttc120
agccatcgca atgcaaaaat aaatatcaat cctccagacg cagtagcagc cgcgctgcgc180
ccaaagtccc aacggccacg cctaacaatt ataaaagtgt tcagcgagag tgttggcggt240
agtgtgaatg ggtgtgcgct ggggggcacg gtggagcggt gtgcaaaatc ggagttgcaa300
accatcggac aagggcattg agtggctacc cgccgcggac tcagcgcggg cgcgctccc360
cgcacacact cacagcagag ttcgcactgg gaagagttaa aaaataaaca ttacaagga420
cgaggaaagc ggccccgctc ccggcgctcc cgggccaggg cgagcgcggc gagggcgca480
ccgaccggtt cgcagcgggg cgggagtcgg aagcgcgcca ggagcgggcg gtcccgggtc540
cttgcggg 548

```

(2) INFORMATION ON SEQ ID NO. 29:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 493 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

gcaagatggc tgcctgaca gcggagattt tgcagcactc cagagcctgc tcaaggcctc 60
ctcgaaagat gttgtcagac agctgtgtca agaaagcttt tccagttcag cccttggtt120
gaaaaaactc ttgatgtta catgttccag cttgtctgtg acccaggagg aggcagagga180
actgctccag gctctgcacc gcctcactag gctggtggca ttccgtgacc tgtcctctgc240
cgaggcaatt ctggctctct ttccagaaaa ttccaccaa aacctcaaaa acctgctgac300
aaagatcatc ctagaacatg tgttactctg gagaaccgaa gccacaggca atcagatctc360
tctgccacgc ctggtcgatc tggactggag agtggatatc aaaacctcct cagacagcat420
cagccgcatg gccgttgccc cacctggcct ggttccagat ggaagggttc aaggaggttc480
ccaggctatg ggg

```

493

(2) INFORMATION ON SEQ ID NO. 30:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1063 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

cgctccccc tccaactctc aaccacttcc tccagccagc gccccagccc tcccgcgcgc 60
cgctgcaggg tcccaggagg cgcagactgt gtccctgaca atgggaacag ccgacagtga 120
tgagatggcc cgggaggccc cacagcacac ccacatcgat gtgcacatcc accaggagtc 180
tgccctggcc aagctcctgc tcacctgctg ctctgcgctg cggccccggg ccaccaggc 240
caggggcagc agccggctgc tgggtggcctc gtgggtgatg cagatcgctg tggggatctt 300
gagtgagtc ctaggaggat ttttctacat ccgcgactac accctcctcg tcacctcggg 360
agctgccatc tggacagggg ctgtggctgt gctggctgga gctgctgcct tcatttacga 420
gaaacggggg ggtacatact gggccctgct gaggactctg ctacgcgctg cagctttctc 480
cacagccatc gctgccctca aactttggaa tgaagatttc cgatatggct actcttatta 540
caacagtgcc tggcgcatct ccagctcgag tgactggaac actccagccc ccaactcagag 600
tccagaagaa gtcagaaggc tacacctatg tacctccttc atggacatgc tgaaggcctt 660
gttcagaacc ctacaggcca tgctcttggg tgtctggatt ctgctgcttc tggcatctct 720
ggccctctg tggctgtact gctggagaat gttcccaacc aaagggaaaa gagaccagaa 780
ggaaatgttg gaagtgagtg gaactagcc atgcctctcc tgattattag tgctggtgc 840
ttctgcaccg ggcgtccctg catctgactg ctggaagaag aaccagactg aggaaaagag 900
gctcttcaac agccccagtt atcctggccc catgaccgtg gccacagccc tgctccagca 960
gcacttgccc attccttaca ccccttcccc atcctgctcc gcttcatgtc cctcctgag 1020
tagtcatgtg ataataaact ctcatgttat tgttcccaaa aaa 1063

```

(2) INFORMATION ON SEQ ID NO. 31:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 472 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

cggctcgagg cggcgcgatg gggcgggggc tggcgcggt cctgttgctc ctccgggctct 60
cggccgggagg gcccgcgcgc gcaggtgcag cgaagatgaa ggtggtggag gagcccaacg 120
cgtttggggg gaacaaccgc ttcttgccctc aggcagtcg cctccaggcc aagagggatc 180
cttcaccggt gtctggacce gtgcatctct tccgactctc gggcaagtgc ttcagcctgg 240
tggagtccac gtacaagtat gagttctgcc cgtccacaa cgtgaccag caccagcaga 300
ccttcgctg gaacgcctac agtgggatcc tcggcatctg gcacgagtgg gagatcgcca 360
acaacacctt cacgggcatg tggatgagg acggtgacga ctgccgttcc cggagccggc 420
agagcaaggg ggagctggcg tgtgcgagcc cgagcaactg cgtctaaggg gt 472

```


(2) INFORMATION ON SEQ ID NO. 32:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2568 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

catctctctg cagtgccttc ctgcctgtg cagcccgccg acccacaggg tcaccctccc 60
tgccgggtgc cagaagcccc ctccagcagg gcctctctcc gtggccccag cttcactctc 120
tccctcagca catgccctgc tggaggcccc agccctccgt ggacagcagg ggccacgtgg 180
agcccgggcc gctcaccgcg gaccagtgct tggccgcctt cttggtgcca aaccctcttc 240
ccccaccag agactgggca gctgtgtctg gttcgttctt tgactaacc acatttgtca 300
tctctagggc aggttggggc tgcgggctga gggggaccgc tggcaccccc cttccctccc 360
ttcttggttc catttccatc catgacaggt acagcatccc aggagcccg cctgaggggc 420
tggacccgag ccggtctgtg acatccctca gccctgctg tcccccttg ggactaacca 480
ctaacctcac ccccaaactc cacgggtgcc cctagctggc ccagagccgg cagtgtgagc 540
ccaagtccgg gctggagccg aggcgggagc agctgtctgg gagtcaaggc tgcagttagc 600
tttcttcatg ggggtgctca gggggtgcca cagaccgaca ggcagcccaa gggcctggag 660
acccctcccc aggcaggtgc tgccccagga ggactgtcct cggaatgaa cctcccggcg 720
gctttggact gaggtcctg tggcctcggt ctctcccca tgaagtggga gcgaggctcc 780
ccaatggtgc ttttggtttt agtgtacgat gtttgcgtg cttcccgcg tggaggcgag 840
agccacccca catcaggatc ggacgtgcta cccctcccg tcccggcctt ggcccagcca 900
gccagccct cgaggctcga tgctgtgcc aaggccagg gcagccagag ggcagctgga 960
tgccacgtg caggggtcaa ggctgggccc tgcagtggg cgggcccga gccccagcag 1020
tttacagacg catggctctt cctcccagag cagccggcag ctacctggac cggaaatgtc 1080
ctcatccctt ccttggggcc aggtctgtcc ctggccttcc tctgtgaacc cctcctttct 1140
ttgtgctggt gtctgggacc aaaaaggggg aatatgggag ggcagagtgg ggaggggagt 1200
ccatgggcct ggggccccaa gccggggcgt ctgagctccc caggcatgac caaacctcag 1260
tgagggggcc tctgcttcag gcccgcctg gctgacattc tgagccccc tcggaggcccc 1320
cgccacagcc aacctgcoca gtctttctc tgggcttgac ccgccaggga gttctccagg 1380
cctagggcca ggagagagg cctggcacc tggcgtgggt gcccgccaaa cgccctgcga 1440
ccgctcagaa gcacaaatgc tgtccatggc cgtgaggctg cctgccaggt gaatggacat 1500
agcgtgagag gcggtgaggc cagggcttcc agcctcgtgc tgtctcggga ctccctgacc 1560
tggtgtgcgt gtgtgcccgt ctgtgacttt ctactacca aggttgaaga aaggaaacgg 1620
ggaaaatcaa aaggggttca aacccacact cagtagggtg aggggagcgc ctgccattgg 1680
ttgtattttt gttctgagtt ttccgtgccc tgttcctaac tactccatcc catgacctcg 1740
ccacacctac tggggcatct ggctgggtgc tgetgcatg gccagcccc actctcacc 1800
tgcacagggg gtcttgagc cccagggccc acagcctcgt tgggaggaca gggtgccct 1860
gggacaaga gggaggagcc caggggctta cctcactgag agtgctccc agcaggcatc 1920
cactacccca gggccccca catgtcatgg caaggttgg agtgaatgg cctggttggg 1980
agcagccctt ggccattgc ccaccaccc atctcactat gcaattcgag ttccaagcaa 2040

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catttgctcc tgccctgggg ccagctctgc cccagccctg agaggggtgg tgaggcagcc2100
ccctggaccc cagaacccca gacaaggggg caggcggggg accagggcct ctctgtggg2160
atctttgttt tgtgtttaac cataatggtt gtgtactgaa ccacttcata tttgttatat2220
ataatatata tatatataat ctcttaaga ctcagcctcc tggtttacct ccccgccctg2280
ggcatctgac ctccccacc ccagtgtgat ttaacatcca ggaactgagg cctgaaccat2340
tttgcatttc cccctctctc agcctctgta gggccatggc tgtatgtact gtcgctgtgt2400
ttttttgttt ttttagaact gggtttgggg gctgattttt atttctttgg gggctttttt2460
tcttgcaaaa tactaaaaat ctctgcaatg taatttctgt ggtttctatt cagcttgggt2520
ttcatgtttt aaaataaatt ttaaaaagca aaaaaaaaaa aaaaaaaa 2568

```

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 239 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

cgcgatggcg gcggggctgg cgcggtcctt gttgctctc gggctctcgg ccggcgggcc 60
cgcgccggca ggtgcagcga agatgaaggt ggtggaggag cccaacgcgt ttgggtgagc120
agcctcgcg gctggcggtt cgagcggggg acggcccggg cccgttcccc gctgaccttg180
ccgcttcccc taggtggaac aaccgttctt tgctcaggc cagtcgcctc caggccaag 239

```

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 482 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
ctccaagctt ggccctggcca acactcggtg ggcagaatga tcacctccgt tgtttcaggt 60
actctgtgtt tatttatgca acagttcatg taaaatggag acgaggccag aagaatcctt120
gagcagacag agccagttgg gctcctaag tgaccttaac cttgcttgat ttgcaagcat180
gtctgaaact ttatttgtgg tatttcttgt aaatgcctat gttaaagaaa cacagaactt240
aagctcaacc aatcagaagc agccaacaaa aacgtaatta gtaactagga cttcctcatg300
ggatagacca aataaggcaa ctgtataact gtgtaactgt ataactgtaa ccaatgaaat360
attatctttg cttttatcta ttgtcctaa aaagcctcct cctcatgttc tctctgggga420
gctccctagc cacttctgga tcaactgctc aataaactct taaatatttt aaaaaaaaaa480
aa
```

(2) INFORMATION ON SEQ ID NO. 35:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 641 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

gagagcagta ggtgttagca gcttggtcgc gacaggggcg ctaggtagag cgccgggacc 60
tgtgacaggg ctggttagcag cgcagaggaa aggcggcttt tagccaggta tttcagtgtc120
tgtagacaag atggaatcat ctccatttaa tagacggcaa tggacctcac tatcattgag180
ggtaacagcc aaagaacttt ctcttgtaa caagaacaag tcatcggcta ttgtggaaat240
attctccaag taccagaaag cagctgaaga aacaaacatg gagaagaaga gaagtaacac300
cgaaaatctc tcccagcact ttagaaaggg gacctgact gtgttaaaga agaagtggga360
gaaccaggg ctgggagcag agtctcacac agactctcta cggaacagca gcactgagat420
taggcacaga gcagaccatc ctctgtctga agtgacaagc cacgctgctt ctggagccaa480
agctgaccaa gaagaacaaa tccaccccag atctagactc aggtcacctc ctgaagccct540
cgttcagggt cgatatcccc acatcaagga cggtgaggat cttaaagacc actcaacaga600
aagtaaaaaa atggaaaatt gtctaggaga atccaggcat g 641

```

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 381 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

aagttgatga cctacgctct tacttctgct tgccaggagt aactgaaagc aaacaccaca 60
gtctgttggt tattagcttt taaaggcttg tcaacattcc ttgttaacaa tttctttttg120
ggtagccttt tataaaatgc gtaggtgatg agtgatccag cagacaaggc ggctcgagcc180
gattcggctc gagcggctcg aggtaaaaga aaaaaaatg tggaggaaaa catggcctac240
tcagctttga tggaagtggc tggttactgc ttaatagaga gaatgctttg gaatcctatg300
ttgaaaataa aaagtgtttg gttgtgcagt tatgcggtca tggtcattcc cagacagttg360
getaaggttt agtggtcctc t 381

```

(2) INFORMATION ON SEQ ID NO. 37:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: Nucleic acid

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

ctggggacag gaagcccctg taccattatg gtcggggcat gaatcccgtc gacaaaccag 60
cctggggccc agaggtaaaa gagagaacaa ggatgaacaa gcagcagaac tctcccttgg 120
ccaagagcaa gccaggcagc acggggcctg agccccccag cccccaggcc tccccagggc 180
ccccaggcct cccctggggc cccaaaacct accacaaatt catggccttc aagtcctttg 240
ccgacctccc ccaccgccct ctgctggtcg acctgacagt agaggagggg cagcggctca 300
aggtcatcta tggctccagt gctggcttcc atgctgtgga tgtcgactcg gggaacagct 360
atgacatcta catccctgtg cacatccaga gccagatcac gccccatgcc atcatcttcc 420
tccccaacac cgacggcatg gagatgctgc tgtgctacga ggacgagggg gtctacgtca 480
acacgtacgg gcgcatcatt aaggatgtgg tgctgcagtg gggggagatg cctacttctg 540
tggcctacat ctgctccaac cagataatgg gctgggggtg gaaagccatt gagatccgct 600
ctgtggagac gggccacctc gacgggggtc tcatgcacaa acgagctcag aggctcaagt 660
tcctgtgtga gcggaatgac aaggtgtttt ttgcctcagt ccgctctggg ggcagcagcc 720
aagtttactt catgactctg aaccgtaact gcatcatgaa ctggtgacgg ggccctgggc 780
tggggctgtc ccacactgga cccagctctc cccctgcagc caggcttccc gggccgcccc 840
tctttccctt ccctgggctt ttgcttttac tggtttgatt tctactggagc ctgctgggaa 900
cgtgacctct gacctctgat gctttcgtga tcacgtgacc atcctcttcc ccaacatgtc 960
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ggaattgagt gggcctagcc cctccccctt tttctccatt tgagaggaga gtgcttgggg1080
cttgaacccc ttaccccaact gctgctgact gggcagggcc ctggaccctt ttatttgcac1140
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agatttttgg ggggtcacca gccactccag gggcagggac catttcttca ttttctgaaa1260
gcactttaat gattcccctg ccccaaaact ccagggaatg gaggggggag cccgccagcc1320
aaaacatgcc ccccatccg gacccccctc tcctcttcta gcccattgcc ttccccgggt1380
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gagcagcaag taaccttct cctccttccc cagtcacccc tcctcaatgt agtggccttg1500
aattgtcttt attaacaaac aggatatcca aggtcgagc 1539

```

(2) INFORMATION ON SEQ ID NO. 38:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2195 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

gctccgagga aggcctgtgg gagtctcgga gacgtgtctg tctgtgaggg gctgggtgca 60
cgtocccagg gctctgggct aggaaggcag cggcgagggt cctccccacg taccctcgc 120
gggcccagcc gagcaacgtg gggcggaagg ggcggcgaa gcccgggctg ggagcgttgg 180
cggccggagt ccagccatg gcggagtctg tggagcgccg gcagcagogg gtccaggagc 240
tggagcggga acttgcccag gagaggagtc tgcagggtccc gaggagcggc gacggagggg 300
gcggccgggt ccgcatcgag aagatgagct cagagggtgg ggattcgaat ccctacagcc 360
gcttgatggc attgaaacga atgggaattg taagcgacta tgagaaaatc cgtacctttg 420
ccgtagcaat agtaggtgtt ggtggagtag gtagtgtgac tgctgaaatg ctgacaagat 480
gtggcattgg taagtgtgta ctctttgatt atgacaaggt ggaactagcc aatatgaata 540
gacttttctt ccaacctcat caagcaggat taagtaaagt tcaagcagca gaacatactc 600
tgaggaacat taatcctgat gttctttttg aagtacacaa ctataatata accacagtgg 660
aaaactttca acatttcag gatagaataa gtaattggtg gttagaagaa ggaaaacctg 720
ttgatctagt tcttagctgt gtggacaatt ttgaagctcg aatgacaata aatacagctt 780
gtaatgaact tggacaaaca tggatggaat ctggggtcag tgaaaatgca gtttcagggc 840
atatacagct tataattcct ggagaatctg cttgttttgc gtgtgctcca ccacttgtag 900
ttgctgcaaa tattgatgaa aagactctga aacgagaagg tgtttgtgca gccagtcttc 960
ctaccactat ggggtgtggt gctgggatct tagtacaaaa cgtgttaaag tttctgttaa1020
atatttggtac tgttagtttt taccttggaat acaatgcaat gcaggatttt tttcctacta1080
tgtccatgaa gccaaatcct cagtgtgatg acagaaattg caggaagcag caggaggaat1140
ataagaaaaa ggtagcagca ctgcctaaac aagagggttat acaagaagag gaagagataa1200
tccatgaaga taatgaatgg ggtattgagc tggatatctga ggtttcagaa gaggaactga1260
aaaatttttc aggtccagtt ccagacttac ctgaaggaaat tacagtggca tacacaattc1320
caaaaaagca agaagattct gtcactgagt taacagtggg agattctggg gaaagcttgg1380
aagacctcat ggccaaaatg aagaatatgt agataatgga ctgggatata ttgtatttct1440
catgttaaag cctcttcctt tgaaattaaa aaaaaatttt aactgataaa acttagggca1500
acattaatta atgtatatc ttacctgaat tgttatactt tttgaaaatc ctgtgacttg1560
cctgtttctc cccgctccaa cgaaatcatt aactctocta aaatgtgttt cattctagta1620
agaaaacctc aaaggatatt gtaggatata aatcttactt gaaaacatag ctgttgaaat1680
gttttgccct tttggagtgg ggaaggaca aatctgatcc tgtaatcttt ttctttccag1740
taatcccttg tgtctgttgc atgaggacat ggacaataaa gtagtatatg atcctcagat1800
acaggagaaa tgacaaggca tacagcttat ccattagagc tggcaagcat ctgctcatta1860
tgtttggaat tgccttctat aagaaaattg cccactacta ctaacttgat caacaatgaa1920
ttcaaaatag ttaacctatg aaataacatc ctctcaaatg tttgctgatg aagtacaagt1980
tgaaatgtag ttattggaaa agtctgtaac ctgtggatca tatatattca aagtgaagaca2040
aaggcaataa aaaagcagct attttcatga atagaaaaaa aaaaaatttc aggaagtata2100
aattatattc tgcaccgaac aaggaaacaga aattattgca tctgtggaag catatatctg2160
ggagttacta ttactttact ggaagggcca agggc

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2195

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1409 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

gtttgctgtc cttttttaaa ggattccaag ccatgtgaaa ttcccttctg gatgtgattc 60
tgggtcgcaa gtccttattt atatgtgagg ctggggaatg ggctgggggt attggcagtc 120
cttttgccagg gcagtgtgtg tgggtgggggt acaccgctgt ggcttagccc aagacactcc 180
cagaggaaaa cactgcagaa ggaactgggt tgcagactgt ggaaggatct gcagttttgt 240
ttttgaccaa aaaaataata ataagtttag tctgaagggc agaggggaata cccaagcccc 300
tgatgcctat gagaagtccc tggacttcaa ccctcctgtt gtttggcctt agcccagagg 360
gagctgctca cctgagcacc cttgggggtg ggcagagagg cagggtggga ttttagagtt 420
agtgtctgtg cgggggcagc cctgagcctg gagttgagac tttgggggtct cttagtttgg 480
aggtgttgag tgcattttgt cccctgcctg gttgagagct tcttggtacc tcttgccacc 540
ccttctcact gccctgaccc aaccccactg gaccttgatg ctgagaggag tgggtgtcctg 600
acggactcag cactcccggc tgatgtattg gatcatagga gagcacttgc tctcctgcct 660
ctgccaggag agggcttggt cctccaactc taggaggcca ggcaagcatg gacaggagcc 720
aaggagcag ggtcattaac tttttcttct ttgcaaagtg ggcacttggc atcagggtcc 780
caatcaccag aaagcaccaa agcccctggc accccacca ctccatccta cccagggacc 840
ccaagtaggc aactgttatg gcagtgggtc cagcccaggc cagcactgcc agcctcctct 900
ccctgcagta ggcaccagct ctacctccc cggcaggcaa tgtcctggct tctcagccca 960
gcaccatctg ttcccctaga cttctcaggg gccagcccag tctggggcac cctttgtttc 1020
cctcatcctc ggctcccaca caggtgacag acccagcaga tagcttctct ctgggaaagg 1080
ttggatgctg ctttacatcc ccttctagcc ctccctccat ccacacacac aggacccac 1140
ccacaccagg tcggcttggt tctcacatgt agggagagag gggagaccaa cccctttgtg 1200
tcttttgaaa tacgaagaaa aatgtgtgtt caggagcatg actccagtgc tgcgctcttg 1260
ggcctagttc agtctgtctt gtctcaaata taggcatttt tgcctcaatt ttattttttt 1320
taaaacattt ttttgggtgt ccggttggtg ttggaataat ttggctaaca ttggtaaaag 1380
gtaagggggg taaaatataa ggtaatttt

```

(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1084 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

ggaatcttta agcaatcata cggggaaaaa gggcccatca ccttcaaagg agccacaatt 60
agactcctca acagacatga ttgaggctgg aagataaggg aatggtatct tcttcaaagc 120
cgaaagaata ggaccacacc tgccaggatt tggttgttta aatataaatc tgatcacccc 180
cctgcttaga acccttctgc tttctattac ccctcattta aaatgtaaac tcttcacctt 240
ggtttatgag aactggttct tgccctcccc ttgaacctca ttaaatggtg atttcttgct 300
aagctccagc ccgagtggtc tctctcagc ttctaatttt gtgctctttc ctgccctttt 360
cctgggcctt ctcagctctc cccccccacc actcttgact cagggtggtgt ccttcttctt 420
caagtcttga caattccogg gcccttcagt ccttgagcag tctacttctg tgtctgtcac 480
cacatcttgt cttttccccc cattgcattt attgcagttt atatatatgc tacttttact 540
tgttcatttc tgtctccccc accaggctgt aaatgagggc agaaaccttg tttgttttat 600
tcaccatcat gtaccaagtg cttggcacat agtgggcctt cattaaatgt ttgttgaata 660
aaagagggaa gaaggcaagc caaccttagc tacaatccta ccttttgata aaatgttcct 720
tttgacaata tacacggatt attatttgta ctttgttttt ccatgtgttt tgcttttatc 780
cactggcatt tttagctcct tgaagacata tcatgtgtga gataacttcc ttcacatctc 840
ccatggtccc tagcaaaatg ctaggcctgt agtagtcaag gtgctcaata aatatttggt 900
tggttggttt gtgagccttg ctgccaagtc ctgcctttgg gtcgacatag tatggaagta 960
tttgagagag agaacctttc cactcccact gccaggattt tgtattgcca tcgggtgccal 1020
aataaatgct catattttatt aaacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1080
aaaa

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1084

(2) INFORMATION ON SEQ ID NO. 41:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2860 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

tcttggtga ttcttttcc ggcagttccc cttatgaggg ttacaactat ggctcctttg 60
agaatgtttc tggatctacc gatggtctgg ttgacagcgc tggcactggg gacctctctg 120
acggttacca gggccgctcc tttgaaccgg taggtactcg gcccagagt gactccatga 180
gctctgtgga ggaggatgac tacgacacat tgaccgacat cgattccgac aagaatgtca 240
ttcgcaccaa gcaatacctc tatgtggctg acctggcacg gaaggacaag cgtgttctgc 300
ggaaaaagta ccagatctac ttctggaaca ttgccaccat tgctgtcttc tatgcccttc 360
ctgtggtgca gctggtgatc acctaccaga cggtggtgaa tgtcacaggg aatcaggaca 420
tctgtacta caacttcctc tgcgcccacc cactgggcaa tctcagcgcc ttcaacaaca 480
tctcagcaa cctggggtac atcctgctgg ggctgctttt cctgctcatc atcctgcaac 540
gggagatcaa ccacaaccgg gccctgctgc gcaatgacct ctgtgccctg gaatgtggga 600
tcccaaaaca ctttgggctt ttctacgcca tgggcacagc cctgatgatg gaggggctgc 660
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gcgtggtctt tggcaaaggg aacacggcgt tctggatcgt cttctccatc attcacatca 900
tcgccaccct gctcctcagc acgcagctct attacatggg ccggtggaaa ctggactcgg 960
ggatcttccg ccgcatcctc cacgtgctct acacagactg catccggcag tgcagcgggc 1020
cgctctacgt ggaccgcatg gtgctgctgg tcatgggcaa cgatcatcaac tggctcgtgg 1080
ctgcctatgg gcttatcatg cgcccaatg atttcgcttc ctacttggtg gccattggca 1140

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tctgcaacct gctcctttac ttcgccttct acatcatcat gaagctccgg agtggggaga1200
ggatcaagct catccccctg ctctgcatcg tttgcacctc cgtggtctgg ggcttcgcgc1260
tcttcttctt cttccagggg ctcagcacct ggcagaaaaa ccctgcagag tcgagggagc1320
acaaccggga ctgcatcctc ctcgacttct ttgacgacca cgacatctgg cacttcctct1380
cctccatcgc catgttcggg tccttctctg tggtgctgac actggatgac gacctggata1440
ctgtgcagcg ggacaagatc tatgtcttct agcaggagct gggcccttcg cttcacctca1500
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cctgggacag ccatggggtg gcatggaacc ttgcagctgc cctctgccga ggagcaggcc1680
tgctcccctg ggacccccag atgttgacca aattgctgct ttcttctcag tgttggggcc1740
ttccatgggc ccctgtcctt tggctctcca tttgtccctt tgcaagagga aggatggaag1800
ggacaccctc cccatttcat gccttgcat ttgcccgtcc tcctcccccac aatgccccag1860
cctgggacct aaggcctctt tttcctccca tactcccaact ccaggggcta gtctggggcc1920
tgaatctctg tcctgtatca gggccccagt tctctttggg ctgtccctgg ctgccatcac1980
tgcccattcc agtcagccag gatggatggg ggtatgagat ttggggggtt ggccagctgg2040
tgccagactt ttggtgctaa ggcctgcaag gggcctgggg cagtgcgtat tctctccct2100
ctgacctgtg ctcagggctg gctctttagc aatgcgtca gcccaatttg agaaccgcct2160
tctgattcaa gaggtgaat tcagaggtca cctcttcac ccacagctc ccagactgat2220
gccagacca ggactggagg gagaagcgcc tcaccccttc ccttccctct ttccaggccc2280
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gtgtttttct cccaaacttg tttttatagc tctgcttgaa gggctgggag atgaggtggg2760
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atttgcatc aataaacaac cagactcaga taacaaaaaa 2860

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(2) INFORMATION ON SEQ ID NO. 42:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2137 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

gtccgctttc gtctccgtcc tgctgccgtt accgccgctg ctgccgccgc ttgcgtcccc 60
cgctccgggtc tgtggtgcag ccgggaccca ggaccatgtc tctgtctcgc tcagaggaga 120
tgcaccgggct cacggaaaaat gtctataaga ccatcatgga gcagttcaac cctagcctcc 180

ggaacttcat cgccatgggg aagaattacg agaaggcact ggcaggtgtg acgtatgcag 240
ccaaaggcta ctttgacgcc ctggtgaaga tgggggagct ggccagcgag agccagggct 300
ccaaagaact cggagacgtt ctcttcaga tggctgaagt ccacaggcag atccagaatc 360
agctggaaga aatgctgaag tcttttcaca acgagctgct tacgcagctg gagcagaagg 420
tggagctgga ctccagggtat ctgagtgtct cgctgaagaa ataccagact gagcaaagga 480
gcaaaggcga cgccctggac aagtgtcagg ctgagctgaa gaagcttcgg aagaagagcc 540
agggcagcaa gaatcctcag aagtactcgg acaaggagct gcagtacatc gacgccatca 600
gcaacaagca gggcgagctg gagaattacg tgtccgacgg ctacaagacc gcaactgacag 660
aggagcgagc gcgcttctgc ttcttggtgg agaagcagtg cgccgtggcc aagaactccg 720
cggcctacca ctccaagggc aaggagctgc tggcgagaa gctgccgctg tggcaacagg 780
cctgtgccga cccagcaag atcccgagc gcgcggtgca gctcatgcag caggtggcca 840
gcaacggcgc caccctcccc agcgccctgt cgccctccaa gtccaacctg gtcatttccg 900
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caaaaaacag ctatgccacc accgagaaca agactctgcc tcgctcgagc tccatggcag 1200
ccggcctgga gcgcaatggc cgtatgcggg tgaaggccat cttctccac gctgctgggg 1260
acaacagcac cctcctgagc ttcaaggagg gtgacctcat taccctgctg gtgcctgagg 1320
cccgcgatgg ctggcactac ggagagagtg agaagaccaa gatgcggggc tggtttccct 1380
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ccgattacgg cgccgcctcc cgggccttcc ccgccagac ggccagcggc ttcaagcaga 1560
ggccctacag tgtggccgtg ccgccttct cccagggcct ggatgactat ggagcgcggt 1620
ccatgagcag cgccgatgtg gaagtggcca gattctgagc cgctgacta gagttagaat 1680
ccctttgccc acgtccagct gaagccgaca gtgaccaacg acaggtctgc cccctcctc 1740
agctgatggc cacatctgca gtgctgccc tctggtggt tccccgccc tcccatgta 1800
gcctgttctg tcatcatctg tgcgttctg ttagagaa atccaggccc cggctgcctg 1860
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ggccgcctct tgagggtaca cgctctggt cacatggcca tggagccttg ggtaccctg 2040
agttaaggga ggacatttg ccagctggtg gctgggagg gagcctggct gccctgctgc 2100
ttctcctgcc taataaacag gcttctcctg caaaaaa 2137

```

(2) INFORMATION ON SEQ ID NO. 43:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2410 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

ttgagcagac acaggtgcag gcagtgggtga ctctacaggc cctgctattc cgggccccttt 60
tgcaacgttg tggcaacaat aaaattttga cgtagccatc ctccatttgg aagtctggtg 120
gctggtttgc cgtggaaatg accctgtttt tattccaga attacctctg ggtttagaga 180
agtggttttt aaacgagtgt gggtaaaaaa aattacctga ggtacttgtc agagtgcag 240
acttctaggt cccaccagc tctcatcaat cagtttagtg aggggtggtg ccaggactct 300
gattttaaac atacccttag aaagattctg atacaggtag aggtgagaag ccctggttta 360
gaggcagctc ggcctccctt catggtggga ccagggccag cagggaatgt cagggccacc 420
cctgaccttc actgtgactt ctggcttgca gagggtggcc cgggaggaga tgggtggagg 480
agctcaacag cgggaaggtg atgtacgcct tctgcagagt gaaggacccc aactctggac 540
tgccaaaatt tgcctcatc aactggacag gcgaggcggt gaacgatgtg cggaaggag 600
cctgtgccag ccacgtcagc accatggcca gcttcctgaa gggggcccat gtgaccatca 660
acgcacgggc cgaggaggat gtggagcctg agtgcacat ggagaaggtg gccaggctt 720
caggtgccaa ctacagcttt cacaaggaga gtggccgctt ccaggacgtg ggaccccagg 780
ccccagtggg ctctgtgtac cagaagacca atgccgtgtc tgagattaaa agggttggta 840
aagacagctt ctgggccaaa gcagagaagg agggaggaga ccgtcggctg gaggaaaagc 900
ggcgggccga ggaggcacag cggcagtgga gcaggagcgc cgggagcgtg agtgcgtgag 960
gctgcacgcc gggagcagcg ctatcaggag cagggtggcg aggccagccc ccaggagacg 1020
tgggagcagc agcaagaagt ggtttcaagg aaccgaaatg agcaggagtc tgccgtgcac 1080
ccgagggaga ttttcaagca gaaggagagg gccatgtcca ccacctccat ctccagtcct 1140
cagcctggca agctgaggag ccccttcctg cagaagcagc tcacccaacc agagaccac 1200
tttggcagag agccagctgc tgccatctca aggccaggg cagatctccc tgctgaggag 1260
ccggcgcccc gactcctcc atgtctggtg caggcagaag aggaggctgt gtatgaggaa 1320
cctccagagc aggagacct ctacgagcag cccccactgg tgcagcagca aggtgctggc 1380
tctgagcaca ttgaccacca cattcagggc caggggctca gtgggcaagg gctctgtgcc 1440
cgtgcocgtg acgactacca ggcagccgac gacacagaga tctcctttga ccccgagaac 1500
ctcatcacgg gcatcgaggt gatcgacgaa ggctggtggc gtggctatgg gccggatggc 1560
cattttggca tgttccctgc caactacgtg gagctcattg agtgaggctg agggcacatc 1620
ttgcccttcc cctctcagac atggcttcct tattgtgga agaggaggcc tgggagttga 1680
cattcagcac tcttccagga ataggacccc cagtaggat gaggcctcag ggctccctcc 1740
ggcttggcag actcagcctg tcacccaaa tgcagcaatg gcctggtgat tcccacacat 1800
ccttctgca tccccgacc ctcccagaca gcttggctct tgcccctgac aggatactga 1860
gccaagccct gcctgtggcc aagccctgag tggccactgc caagctgcgg ggaagggtcc 1920
tgagcagggg catctgggag gctctggctg ccttctgcat ttatttgct ttttctttt 1980
tctcttgctt ctaaggggtg gtggccacca ctgtttagaa tgaccttgga gaacagtga 2040
cgtagagaat tgtttttagc agagtttgtg accaaagtca gagtggatca tgggtggttg 2100
gcagcagggg atttgtcttg ttggagcctg ctctgtgctc cccactccat ttctctgtcc 2160
ctctgcctgg gctatgggaa gtggggatgc agatggccaa gctcccaccc tgggtattca 2220
aaaacggcag acacaacatg ttcttcacg cggctcactc gatgcctgca ggccccagtg 2280
tgtgcctcaa ctgattctga cttcaggaaa agtaacacag agtggccttg gcctgtgtc 2340
ttcccctatt ttctgtccca gctcatccgt gtctctgaag aacaaatatg cttttggacc 2400
aaaaaaaaa

```

2410

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2333 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

tgaaaaatgc	ggacagtata	ttcagaaagg	ctattccaag	ctcaagatat	ataattgtga	60
actagaaaaat	gtagcagaat	ttgagggcct	gacagacttc	tcagatacgt	tcaagttgta	120
ccgaggcaag	tcggatgaaa	atgaagatcc	ttctgtggtt	ggagagttaa	agggtcctt	180
tcggatctac	cctctgccgg	atgaccccag	cgtgccagcc	cctcccagac	agtttcggga	240
attacctgac	agcgtcccac	aggaatgcac	ggttaggatt	tacattgttc	gaggcttaga	300
gctccagccc	caggacaaca	atggcctgtg	tgacccttac	ataaaaaataa	cactgggcaa	360
aaaagtcatt	gaagaccgag	atcactacat	tcccaacact	ctcaaccagg	tctttggcag	420
gatgtacgaa	ctgagctgct	ctttacctca	agaaaaagac	ctgaaaattt	ctgtctatga	480
ttatgacacc	tttaccggg	atgaaaaagt	aggagaaaca	attattgatc	tggaaaaccg	540
attcctttcc	cgctttgggt	cccactgcgg	gagtagcag	gagtactgtg	ttctcggagt	600
caatacctgg	cgagatcaac	tgagaccaac	acagctgctt	caaaatgtcg	ccagattcaa	660
aggcttccca	caacccatcc	tttccgaaga	tgggagtaga	atcagatatg	gaggacgaga	720
ctacagcttg	gatgaatttg	aagccaacaa	aatcctgcac	cagcacctcg	gggcccctga	780
agagcggctt	gctcttcaca	tcctcaggac	tcaggggctg	gtccctgagc	acgtggaaac	840
aaggactttg	cacagcacct	tccagcccaa	catttcccag	ggaaaacttc	agatgtgggt	900
ggatgttttc	cccagagttt	tggggccacc	aggccctcct	ttcaacatca	caccccgga	960
agccaagaaa	tactacctgc	gtgtgatcat	ctggaacacc	aaggacgtta	tcttggacga	1020
gaaaagcatc	acaggagagg	aaatgagtga	catctacgtc	aaaggctgga	ttcctggcaa	1080
tgaagaaaaac	aaacagaaaa	cagatgtcca	ttacagatct	ttggatggtg	aagggaattt	1140
taactggcga	tttgttttcc	cgtttgacta	ccttccagcc	gaacaactct	gtatcgttgc	1200
gaaaaaagag	catttctgga	gtattgacca	aacggaattt	cgaatcccac	ccaggctgat	1260
cattcagata	tgggacaatg	acaagttttc	tctggatgac	tacttgggtt	tcctagaact	1320
tgacttgctg	cacacgatca	ttcctgcaaa	atcaccagag	aaatgcaggt	tggacatgat	1380
tccggacctc	aaagccatga	acccccttaa	agccaagaca	gcctccctct	ttgagcagaa	1440
gtccatgaaa	ggatggtggc	catgctacgc	agagaaaagt	ggcgcccgcg	taatggctgg	1500
gaaagtggag	atgacattgg	aaatcctcaa	cgagaaggag	gccgacgaga	ggccagccgg	1560
gaaggggctg	gacgaaccca	acatgaaccc	acatctggac	ttaccaaatc	gaccagaaac	1620
ctccttctct	tggttcacca	acccatgcaa	gacctgaag	ttcatogtgt	ggcgccgctt	1680
taagtgggtc	atcatcggtc	tgtgttctct	gcttatcctg	ctgctcttcg	tggcgtgctt	1740
cctctactct	ttgccgaact	atttgtcaat	gaagattgta	aagccaaatg	tgttaacaa	1800
gcaaaggctt	catttcaaga	gtcatccagc	aatgagagaa	tctgcctct	gtagaccaac	1860
atccagtgtg	attttgtgtc	tgagaccaca	ccccagtagc	aggttacgcc	atgtcaccga	1920
gccccattga	ttcccagagg	gtcttagtcc	tggaaagtca	ggccaacaag	caacgtttgc	1980
atcatgttat	ctcttaagta	ttaaaagtgt	tattttctaa	agtttaaatc	atgtttttca	2040
aaatatTTTT	caagggtggc	ggttccattt	aaaaatcatc	tttttatatg	tgtcttcggg	2100
tctagacttc	agcttttggg	aatttgctaaa	tagaattcaa	aaatctctgc	atcctgaggt	2160
gatatacttc	atatttgtaa	tcaactgaaa	gagctgtgca	ttataaaatc	agttagaata	2220
gttagaacia	ttcttattta	tgccacaaac	cattgctata	ttttgtatgg	atgtcataaa	2280
agtctattta	acctctgtaa	tgaactaaaa	taaaaatggt	tcacctttaa	aac	2333

(2) INFORMATION ON SEQ ID NO. 45:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1612 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

gtcttctttt ttttctttt ttttttttt ttttttttc cctgtggaag tgcttttatt 60
agcagtaagg ctgacgttac aaaaaattct cagagcttca taggacaagg tagtacaagt 120
atggatgata caggactgag gaacggggga cggctcaaaa gaaatcaaca tcgtctgggg 180
catccaggtc ccgatattcc acaatggccc ttgggtctcc acgaaccatc ctgttgcgag 240
gtttcccagg ataacctccc tggcctcgga aggcatacata gttccctcga ccagaccat 300
acggggcatg ggggtatgga gggcctcctg tggggactgc agggcggaca gcaccagctc 360
catagcccaa gatcgggggc cggggctgac catagggcat caggccctgg ggagtctggt 420
gtgggtaggg gagtcctggg gtcaaacctg gggggagtat ctgggcgggc ccaggtggt 480
gggctggctt gatctcaggc agagctgggc gcttagcatc agtgaggaag ttgttaaaaa 540
acgcgacttc ctttttctac tcttcaattt tctctgcatg cttgttgaag atatgtttgc 600
gcacaaactc aggacccttg aatttcttgc cactgagagg acacagccac ttatccttgc 660
ccagttcctg cgtgttggag gtgacgaact tctccacttc ctgctctggg tctttgcgcc 720
ccatcttctg ggctcttccc tctgagagtg actcccgcac actcagcaac ggcgtgagct 780
tctctcaaaa agtcttctgc cactccagca cttccccgtg actgatgcgg ttgggtggca 840
tgggcccccg aacgtggatg atcccacagc gattgggcat ctgctcctcg ttgggggtact 900
cacagggtgt gtaataatcc aaggaatgca cgatgcgcag gtaaaggagg agcttgtcca 960
agaccttaat caacttctca tcccgtccca cgttgatctc tgccgggttc cttccttag1020
gaggctcctc aggaggagcg ccccgcgtgc tcccagcag ctccctcctc tcggcgctta1080
cttctcgat caggtagtcg gtgatattct tcaagatcgg gttttgcgag ggcaggctcg1140
tgggcagggg aggcgtccct ggttctgagg cccaaagctg tgcctgtca tccagcgtgt1200
ggatcagctt ggccgccagc ttgatgtcgt tgccgacaat ctgcttgtgc tgggtgatgc1260
cgttgatgtt gcgaacgcgc cgggtcaggc ccctgttcac accagggtc agctcacact1320
cccggagacg gatgttctgc aggttccaac agatctctt aatgttaaca ctgcggctga1380
aggtcaccca gccacgacgg aaaaacctcc tctctggctg gggctctgag agcgcacccc1440
gcataaagcc tgggtacctt ttacaaaggg agatgatctc ggccgggag atgttgggcg1500
cgatgttgcg catgaagagg gagcaggctc tatgcagcgg ccgcggcttg cactccagcc1560
ccgcggcgctc cttgggcttc tccattctt cttccttggg cttctccttc tc 1612

```

(2) INFORMATION ON SEQ ID NO. 46:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

gaaagctctg gctttcaggc tataggaaga gcagaagatg atgccagaag ttgctggggt 60
aaaaccagcg agtccacccg tccttaccag ctctcagaa ggcggagacc gaccctgata 120
acttaccgga tatttcgtca cagaagacac aaagacacat ccagcgggga ccacctcacc 180
tgcagattag accccaagc caaagacctg aaggatggga cccaggagga ggccacaaaa 240
aggcaagaag cccctgtgga tccccgcccg gaaggagatc cgcagaggac agtcatcagc 300
tggaggggag cggatgatcg gcctgagcag ggcaccgagc tcccttcaag aagagcagaa 360
gtgcccacca agcctcccc tccaccggcc aggacacagg gcacaccagt gcatctgaac 420
tatcgccaga agggcgtgat tgacgtcttc ctgcatgcat ggaaaggata ccgcaagttt 480
gcatggggcc atgacgagct gaagcctgtg tccaggctct tcagtgagtg gtttggcctc 540
ggtctcacac tgatcgacgc gctggacacc atgtggatct tgggtctgag gaaagaattt 600
gaggaagcca ggaagtgggt gtcgaagaag ttacactttg aaaaggacgt ggacgtcaac 660
ctgtttgaga gcacgatccg catcctgggg gggctcctga gtgcctacca cctgtctggg 720
gacagcctct tcctgaggaa agctgaggat tttggaaatc ggctaattgc tgccttcaga 780
acaccatcca agattcctta ctcgatgtg aacatcggtg ctggagttgc ccaccgcca 840
cgggtggacct ccgacagcac tgtggccgag gtgaccagca ttcagctgga gttccgggag 900
ctctcccgtc tcacagggga taagaagttt caggaggcag tggagaaggt gacacagcac 960
atccacggcc tgtctgggaa gaaggatggg ctggtgcccc tgttcatcaa taccacagt 1020
gggcctgttt caccacctg gggcgtatct cacggtgggg cgccaggggc cgacagctta 1080
ttattgagtt acctgtttga aaggca
1106

```


(2) INFORMATION ON SEQ ID NO. 47:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1370 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

gcggtggcga ggggcgtaac ggttgttgta gtcggcccc ctcttggtg gtccagccac 60
attaaccggc aggatgtcgg aggtgcggt gccaccgcta cgcgccttg acgactttgt 120
tctggggctg gcgcgtctgg cggctccgga tccatgcgac ccgcagcgat ggtgccaccg 180
cgtcatcaac aacctcctct actaccaaac caactacct ctctgcttcg gcatcggcct 240
cgctctcgcc gggtacgtgc ggccacttca tacgctcctg agcgcgctgg tagtggcggt 300
ggccctcggc gtgctggtgt gggcagctga gaccgcgca ctgtgcgccg ctgccgccgc 360
agccaccctg cagcctgcct ggccgcagtg cttgccgtcg gcctcctggt gctctgggtc 420
gcgggcggcg cttgcacctt cctgttcagc atcgccgggc cggtgcttct gatcctggtg 480
cacgcctcgt tgcgcctgcg caaccttaag aacaagattg agaacaagat cgagagcatt 540
ggtctcaagc ggacgccaat gggcctgcta ctagaggcac tgggacaaga gcaggaggct 600
ggatcctagg cccctgggat ctgtaccag gacctggaga ataccacccc acccccagcc 660
cataattggg acccagagcc ctttcccagc acttaaaaca ggagcctaga gccccctgcc 720
caaacaaaac aggacatctg tgaccgcctt acccccacgc cagcccaaaa ctaagatatc 780
cctcaccccc agccccatt acctagggac aagagtcttc ccagccttg aacctaggac 840
caagagccac ctacatccag ccccaaaact ggggcttcag gccagagcat ccattggcaa 900
tttcaaattg tgaaccaga gacactcca tccacccttc tccatgctca tccccaaact 960
ggggcctgga gcaaggcact ctcaaatctt gaaccctgga ccaaagcttt tccagacccc1020
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ccatgcccct gtgtggatgg agtcgggtat cctgactgtt ggacccttg tccaggtgat1140
cccgacctc accagtcca tttgctccc tccagctctg cttaggcatt ttgcccctca1200
ccccaatgtt ccacaccatc gacaaccaag gggtaggtg gggacaggcc tcagcaggga1260
atggggcgta tatgttagtg ttgctgcaac aataaagcct gttgcatctc tcatgccaaa1320
aaaaaaaaaa aagtcgaccg gccgcaaata tagtagtagt agtcgtccgc 1370

```

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 617 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```
ctcgtagttt attaaatgat gtacaatttg gccagtttgg agatgaccca aaggaggaag 60
taatggttct ggagagaatc ttactggcag accatcaagg ttgatttaca ggtagaacat120
ccataccagt tcctactaaa atatgcaaag caactcaaag gtgataaaaa caaaattcaal80
aagtgggttc aaatggcatg gacatttgta aatgacagtc tctgcaccac cttgtcactg240
cagtgggaac cagagatcat agcagtagca gtgatgtatc tcgcaggacg tttgtgcaaa300
tttgaaatac aagaatggac ctccaaaccc atgtatagga gatggtggga gcagtttgtt360
caagatgtcc cggtcgacgt tttggaagac atctgccacc aaatcctgga tctttactca420
caaggaaaac aacagatgcc tcatcacacc ccccatcagc tgcaacagcc cccatctcct480
gagcctccca ccccgctgcc tgggcctgtg ggttgctggg cctcccacct caaggagggg540
aaggttgtag agcccgaacc cgtggagcaa tgccctgtct ggcctccaaa accaaaataa600
aactgggtca ctttaaa                                     617
```

(2) INFORMATION ON SEQ ID NO. 49:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1899 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

tgtgtgaggc ccaacagcgg aatcatcgat gcaggggcct gaattaatgt atctgtgatg 60
ttacagcctt tcgattatga tccaatgag aaaagtaaac acagggttat gttcagtcta 120
tgtttgctcc aactgacact tcagatatgg aagcagtatg gaaggaggca aaaccggaag 180
accttatgga ttcaaaactt agatgtgtgt ttgaattgcc agcagagaaat gataaaccac 240
atgatgtaga aataaataaa attatatcca caactgcatc aaagacagaa acaccaatag 300
tgtctaagtc tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 360
gtaagaggct gcaagggtgaa gttcagaggc tacgggagga gaacaagcag ttcaagggaag 420
aagatggact gcggatgagg aagacagtcg agagcaacag ccccatctca gcattagccc 480
caactgggaa ggaagaaggc cttagcaccg ggctcttggt tctggtggtt ttgttcttta 540
tcgttggtgt aattattggg aagattgcct tgtagaggta gcatgcacag gatggtaaat 600
tggattggtg gatccaccat atcatgggat tttaatttat cataaccatg tgtaaaaaa 660
aattaatgta tgatgacatc tcacaggtct tgcctttaa ttaccctcc ctgcacacac 720
atacacagat acacacacac aaatataatg taacgatctt ttagaaagt aaatgtat 780
agtaactgat tgagggggaa aagaatgatc tttattaatg acaagggaaa ccatgagtaa 840
tgccacaatg gcataattga aatgtcattt taaacattgg taggccttgg tacatgatgc 900
tggattacct ctcttaaaat gacacocctc ctgcctgtt ggtgctggcc cttggggagc 960
tggagcccag catgctgggg agtgcggtca gctccacaca gtagtcccca cgtggcccac1020
tcccggccca ggctgctttc cgtgtotcca gttctgtcca agccatcagc tccttgggac1080
tgatgaacag agtcagaagc ccaaaggaat tgcactgtgg cagcatcaga cgtactcgtc1140
ataagtgaga ggcgtgtgtt gactgattga cccagcgctt tggaaataaa tggcagtgtc1200
ttgttcactt aaagggacca agctaaattt gtattggttc atgtagtga gtcaaaactgt1260
tattcagaga tgtttaatgc atatttaact tatttaatgt atttcattct atgttttctt1320
attgtcacia gagtacagtt aatgctgcgt gctgctgaac tctgttgggt gaactggtat1380
tgctgctgga gggctgtggg ctctctgtgc tctggagagt ctggtcatgt ggaggtgggg1440
tttattggga tgctggagaa gagctgccag gaagtgtttt ttctgggtca gtaaataaca1500
actgtcatag ggagggaaat tctcagtagt gacagtcac tctaggttac cttttttaat1560
gaagagtagt cagtcttcta gattgttctt ataccacctc tcaaccatta ctcacacttc1620
cagcgcacag gtccaagtct gagcctgacc tccccttggg gacctagcct ggagtcagga1680
caaattggatc gggctgcaga gggttagaag cgagggcacc agcagttgtg ggtggggagc1740
aagggaagag agaaactctt cagcgaatcc ttctagtact agttgagagt ttgactgtga1800
attaatttta tgccataaaa gaccaaccca gttctgtttg actatgtagc atcttgaaaa1860
gaaaaattat aataaagccc caaaattaag aaataaaaa 1899

```

(2) INFORMATION ON SEQ ID NO. 50:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

agaatgtcgg gcggtgctgc gaggcccaag cccgggcccgg ggccgcctcc ctcaacgcct 60
cccttgacgg cctccacaac gcactcttcg ccactcagcg cagcttggag cagcaccagc 120
ggctcttcca cagcctcttt gggaaacttc aagggctcat ggaagccaac gtcagcctgg 180
acctggggaa gctgcagacc atgctgagca ggaaagggaa gaagcagcag aaagacctgg 240
aagctccccg gaagagggac aagaaggaa cggagccttt ggtggacata cgggtcacag 300
ggcctgtgcc aggtgccttg ggcgcggcgc tctgggaggg aggatccctt gtggccttct 360
atgccagctt ttcagaaggg acggctgccc tgcagacagt gaagttcaac accacataca 420
tcaacattgg cagcagctac ttccctgaac atggctactt ccgagcccct gagcgtggtg 480
tctacctgtt tgcaagtggc gttgaatttg gccaggggcc aggcaccggg cagctggtgt 540
ttggaggtca ccacgcgact ccagtctgta ccactgggca ggggagtggg agcacagcaa 600
cggctcttgc catcggaact ctgcagaagg gtgagcagat atggtttgag ttaaccagg 660
gatcaataac aaagagaagc ctgtcgggca ctgcatttgg gggcttcctg atgtttaaga 720
cctgaacccc agccccaatc tgatcagaca tcatggactc gccagctctt cctcggcctg 780
gggctctggc caaggatggg ctggagggtc ttcagttggt ctgtctcttc cctggaaacc 840
ttctgcaaa atggtgtggt gtacgtggct tccctgtaac cacatggggc ttggccattt 900
ctccatgatg agaaggactg gaatgcttct cggggcagga catggtccta ggaagcctga 960
accttggtct ggcattgcct ctccagacagc acggcctggg ctccaactct tcaccacacc 1020
ctgtattcta caacttcttt ggtgttttgc tctcctgtg gttggaaact tctgtacaac 1080
actttaaaact tttctcttgc ttctcttctt ctctccctt atcgtatgat agaaagacat 1140
tcttccccag gaggaatgtt taaaatggag gcaacatttt ggccaacatt ggaaagcact 1200
agagggcaat gggattaaac caacctgctt ggtctctatt agtcagtaat gaagacgaca 1260
gcctggccaa ccaagggaaa ggaaattagt atcttttagt tcagtcattc cttgtagggg 1320
tatgggtttt agcttgtggc ccccaccgaa aagattcatc ttggattgtt aatgcctatt 1380
attcccaca ttaagggg

```

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

tttggcatca tttacaattt catagaatta ctgtgaaggc ctttctagtt gagatgttgg 60
ggtattttggg attctaattg ttaacccag aagaaggtaa tttagcttgt atttatttaa 120
aaccattta gccttttact tatactctgt agaattccag tgatcatcct aataaggat 180
atttcagaat aatttttttt tccttcagaa taacttagaa tcagatgcta taagggtcc 240
taggagcagt gtgaaatttc cgtaaagata aatttgaatg ttgtaaccaa gtttatatta 300
aaccaagagg ccatttccaa tatgattttt tgtttctttt taacttgta agtccctaag 360
agattacatg ctagggtctg agtcatttct attgtagata atgatggccc acacagtcac 420
cttcaactat ccacataagc taggctttcc gcttttgcca cggacagtgt gaccaagata 480
tttccagagt aaataaccba ccacaacctt ggtaattcct cttttcttct taagctccag 540
gaagcgaag cagaaggact cttttcagac tgccctctgt agcctacatt gcagctttcc 600
aaaacaggca gctagcactg ggaaagccca tgtggtgacc ccataatttt ctgagggtct 660
tcttttccat ggtgttactt tattatcaga aagtaaattc agaaaacagg tcttgccctt 720
agcagacaag aaccacacca gtttcttgta aaggtaacgg atacattggg attcaggagt 780
gacacagagg tccagcccca gaacttgtaa ggattttgtt tgaacactga gcagatgcct 840
cctccctgcc acccatcaca ctagttaggg ctggccatga attctatgcc agagtcactc 900
ctgcagtctg ctagggtatg gccttcttat cccactctcg cacacatccc agtctagtct 960
ttgccttcac agagtcctcc ttgacacccc tgacttaatg atagttgctg ttttggagta1020
gaattgatca ggtttaagtc atcctgctca ggttgggcat agtggctcat gcctgtaatc1080
tcagcacttt gggaagccaa agtgggagga ttgcttgagc ccaggagtcc caaacatcc1140
tgggcaacag agggagaccc tgtctctacc aagaaaaaaa aaaaaaaaaa aaagttaaaa1200
aaacaattag ctggacctgg tggcgacac tcagtaggct gaggtgaaag gattccttta1260
acatgggaga ctgaagatgc agtgagccat gaatcagcaa ctgcacacca gtatgagaga1320
aaaagtggaa ccctatcaca

```

(2) INFORMATION ON SEQ ID NO. 52:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 315 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

atcagcacat caattgcagc attgtggcta ccaggggggc aggatgcggg cgggtggagcc 60
ctctggcctt tgtgtggtag ccgaggactc tgtgtcagcg accgttttcc gggaaacttc120
cgggcgagac tcacatcttg gaaattcaaa tactcaatag ctctcgaatt ctaggaatct180
tgagaagagg cctggattaa ggattcagac gtgggccctc agatggctat ggcattgctg240
gttctaccaa cgtgacaggt gatcaagtta agaagctgga cgtcctctcc aacgacctgg300
gtatggaaca ggta                                     315

```

(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1162 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

cggctcgagc ggctcgagat tcgaggctcgt ggtgggtcttg gaagagcgtc gagggggccg 60
tggacgtgga atgggcccag gagatggatt tgattctcgt ggcaaactg aatttgatag 120
gcatagtgga agtgatagat ctggcctgaa gcacgaggac aaacgtggag gtagcggatc 180
tcacaactgg ggaactgtca aagacgaatt aacagagtcc cccaaatata ttcagaaaca 240
aatatcttat aattacagtg acttggatca atcaaatgtg actgaggaaa cacctgaagg 300
tgaagaacat catccagtgg cagacactga aaataaggag aatgaagttg aagaggtaaa 360
agaggagggg ccaaagaga tgactttgga tgagtggaa gctattcaaa ataaggaccg 420
ggcaaaagta gaatttaata tccgaaaacc aaatgaaggt gctgatgggc agtggaaaga 480
gggatttggt cttcataaat caaagagtga agaggctcat gctgaagatt cggttatgga 540
ccatcatttc cggaagccag caaatgatat aacgtctcag ctggagatca attttgga 600
ccttgccgc ccaggacgtg gcggcagggg aggacgaggt ggacgtgggc gtggtggcg 660
cccaaaccgt ggcagcagga ccgacaagtc aagtgttct gtcctgatg tggatgacc 720
agaggcattc ccagctctgg cttaactgga tgccataaga caaccctggt tcctttgtga 780
acccttctgt tcaaagcttt tgcatgctta aggattccaa acgactaaga aattaaaaaa 840
aaaaagactg tcattcatac cattcacacc taaagactga attttatctg ttttaaaaat 900
gaacttctcc cgctacacag aagtaacaaa tatggtagtc agttttgtat ttagaaatgt 960
attggtagca gggatgtttt cataattttc agagattatg cattcttcat gaatactttt 1020
gtattgtgc ttgcaaatat gcatttccaa acttgaaata taggtgtgaa cagtgtgtac 1080
cagttaaaaa aatcacaaaa aaaaaaatt ttaattaagt atttagaagt tcccccaatt 1140
acaaactggt tttaaatatt gg
1162

```

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1826 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

cggctcgagg cccccgcctt gttcgccccg cgccaccggc ccgcgccccg ccatggagga 60
cctggatgcc ctgctctctg acctggagac taccacctcg cacatgccaa ggtcaggggc 120
tcccaaagag cgccctgcgg agcctctcac ccctcccca tcctatggcc accagccaca 180
gacaggggtc ggggagtcct caggagcctc gggggacaag gaccacctgt acagcacggt 240
atgcaagcct cggcccccaa agcctgcagc cccggcggcc cctccattct cctcttccag 300
cgggtgtctt ggtaccgggc tctgtgagct agatcggttg cttcaggaac ttaatgccac 360
tcagttcaac atcacagatg aaatcatgtc tcagttccca tctagcaagg tggcttcagg 420
agagcagaag gaggaccagt ctgaagataa gaaaagaccc agcctccctt ccagcccgtc 480
tcctggcctc ccaaaggctt ctgccacctc agccactctg gagctggata gactgatggc 540
ctcactctct gacttccgcg ttcaaaacca tcttccagcc tctgggcca ctcagccacc 600
ggtggtgagc tccacaaatg agggctcccc atccccacca gagccgactg gcaagggcag 660
cctagacacc atgctggggc tgctgcagtc cgacctcagc cgccgggggtg ttccaccca 720
ggccaaaggc ctctgtggct cctgcaataa acctattgct gggcaagtgg tgacggctct 780
gggcccgcgc tggcaccctg agcacttcgt ttgcccaggc tgttccaccg ccctgggagg 840
cagcagcttc ttcgagaagg atggagcccc cttctgcccc gactgctact ttgagcgtt 900
ctcgccaaga tgtggcttct gcaaccagcc catccgacac aagatggtga ccgcttggg 960
cactcactgg caccagagc atttctgctg cgtcagttgc ggggagccct tcggagatga 1020
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cccgcgtgc cagggctgcc agggcccat cctggataac tacatctcgg cgctcagcgc 1140
gctctggcac ccgactgtt togtctgcag ggaatgcttc gcgcccttct cgggaggcag 1200
ctttttcgag cacgagggcc gcccgttgtg cgagaaccac ttccacgcac gacgcggctc 1260
gctgtgcgcc acgtgtggcc tccctgtgac cggccgctgc gtgtcgcccc tgggtcgccg 1320
cttccacccg gaccatttca catgcacctt ctgcctgcgc ccgctcacca aggggtcctt 1380
ccaggagcgc gccggcaagc cctactgcc a gccctgcttc ctgaagctct tcggctgaca 1440
gccgctcgg ctcgccctct ccccgaggag ccgcgcctc ccggaaaagc cgggtcctcc 1500
agaccccgag gccttgcctc cagagcggga ggccccacc actggagagc ccgcccccta 1560
aggtactatg agtcctcagg ggtcaagttc agaaacggcc cagccagacc taaaccaca 1620
cgccacaaa gtggattgca cacagacaag aactcccggt cgggcctcca ctctattccc 1680
acccttgagg gagccccctt actgggggag ggtccttgca attccagcga atcgaggcc 1740
aggccaggac gtccttgctc cctgcacctt cactgttctg tgcaactttt ctacctacat 1800
aaacacacgc attccacctc aaaaaa

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1826

(2) INFORMATION ON SEQ ID NO. 55:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1114 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

gatgaagtag atgactttga ggacttcac ttcagccact tctttggaga caaagcactg 60
aagaagaggt caggaagaa ggacaagcac tcacagagcc caagagctgc ggggccagg 120
gaggggcaca gcatagggg ctgacaccct gcccacagg gaatggcctt ggcctggccc 180
agcccaagat cccagcgta tctaactcct ggagggtgga ctctgtcctg gcttgtttg 240
tgtcctcaga tatctttcac acagtagagc aaaatcacca gccctgcaact gatgtcactt 300
tatgtagaaa aaggccttag ctggacctgc gttgccgtct atgcaaatgc atgcaaatac 360
tccaggccct gggatgtggg cttgtgtttt gtcactgtga agggggagat gggagaggag 420
cctgttttgg ggtgggtct ggggaaggca atctgattct gaagctaaag agctttcatc 480
ctcttgagtg tatgtcccca tagtgggcc cttgaccac atgctgaccg gtgccttggg 540
atgtgactag agttgctggc tggaggccca gcacgaggac ttaccctggg gttttgtag 600
gtttggaagc agctgtccct agggggtgaa gtccccccc tttttttttt tttaccctg 660
cttctccac ggccttcacct ccctatgtga actgtagact cagatcccaa taaagtgtg 720
ttgcagctat gatgctaggt ggtttctaag cacaggggac accccacacc ccctgcctga 780
atggatgggt ccaccccagg cactggtact tgcccccttg ttctgtatcc ccctttgccc 840
ttgccttgcc cttccaacaa accctaggcc cttgagaagc tgatacttct ccttttgctc 900
acagctgcct tggccccacc cctgggagat gtagcaaatt gagtgtgggt tttggagtct 960
gagcctcagg ctcaaatcca ggccaagtga tcttgggcaa gttaatctct gggaaactttg 1020
ggtttcttat cctcaaaaaa ggcgatggaa gggctgggga agtgattaaa taaaagcaac 1080
gcaagaaaaa aaaaaaaaaa aaaaaaaaaa aaaa

```

(2) INFORMATION ON SEQ ID NO. 56:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

ctcgagccgt gcaagtggaa taacaogggc tgccaggccc tgcccagcca agaacgaagg 60
ccccagcaag gccttcgtga actgtgacga gaacagccgg cttgtctccc tgaccctgaa 120
cctggtgacc agggctgatg agggctggtg ctggtgtgga gtgaagcagg gccacttcta 180
tggagagact gcagccgtct atgtggcagt tgaagagagg aaggcagcgg ggtcccgcga 240
tgtcagccta gcgaaggcag acgctgctcc tgatgagaag gtgctagact ctggttttcg 300
ggagattgag aacaaagcca ttcaggatcc caggcttttt gcagaggaaa aggcggtggc 360
agatacaaga gatcaagccg atgggagcag agcatctgtg gattccggca gctctgagga 420
acaaggtgga agctccagag cgctggtctc caccctgggtg cccctggggc tgggtgctggc 480
agtgggagcc gtggctgtgg ggggtggccag agcccgccac aggaagaacg tcgaccgagt 540
ttcaatcaga agctacagga cagacattag catgtcagac ttcgagaact ccagggaatt 600
tggagccaat gacaacatgg gagcctcttc gatcactcag gagacatccc tcggaggaaa 660
agaagagttt gttgccacca ctgagagcac cacagagacc aaagaaccca agaaggcaaa 720
aaggtcattc aaggaggaag ccgagatggc ctacaaagac ttctgtctcc agtccagcac 780
cgtggccgcc gaggcccagg acggccccc ggaagcctag acggtgtcgc cgcctgtccc 840
ctgcacccat gacaatcacc ttcagaatca tgtcgatcct ggggccctca gctcctgggg 900
acccactccc ctgctctaac acctgcctag gtttttctta ctgtcctcag aggcgtgctg 960
gtcccctcct cagtgcacac aaagcctggc ctaattgttc ctattgggga tgagggtggc1020
atgaggaggt ccacttgca acttctttct gttgagagaa cctcaggtac ggagaagaat1080
agaggtcctc atgggtccct tgaaggaaga gggaccaggg tgggagagct gattgcagaa1140
aggagagacg tgcagcgccc ctctgcaccc ttatcatggg atgtcaacag aatttttccc1200
tccactccat ccctccctcc cgtccttccc ctcttcttct ttccttccat caaaagatgt1260
atttgaattc atactagaat tcaggtgctt tgctagatgc tgtgacaggt atgccacca1320
cactgtcac agcctttctg aggacaccag caaagaagc cacagctctt cttggcgtat1380
ttatactcac tgagtcttaa cttttcacca ggggtgctca cctctgcccc tattgggaga1440
ggtcataaaa tgtctcgagt cctaaggcct taggggtcat gtatgatgag catacacaca1500
ggtaattata aaccacatt cttaccattt cacacataag aaaattgagg tttggaagag1560
tgaagcgttt ttctttttct tttttttttt tgagacggag gtcttctact tcgcccaggc1620
tggagtgcag tggcgcaatc tcgg
1644

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(2) INFORMATION ON SEQ ID NO. 57:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2184 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

tgcaagtggc	agagtgaacct	ggtataagg	agagggcatc	accttgcccc	ctgtgctgac	60
tcctgccctt	gtgcgagggg	agtcacatccc	gatccggctc	ttcctggccg	ggtatgagct	120
cacgcccacc	atgcgggaca	tcaacaagaa	gttctctgtg	cgctattacc	tcaacctggt	180
gctgatagac	gaggaggagc	ggcgctactt	caagcagcag	gaagtgggtg	tgtggcggaa	240
gggtgacatc	gtacggaaga	gcatgtccca	ccaggcggcc	atcgccctac	agcgctttga	300
gggcaccacc	tccttgggtg	aggtgcggac	ccccagccag	ctgtctgaca	acaactgcag	360
gcagtagggc	cccaggggccg	agaagatgct	gggcacccac	ccagcacccc	catctaccaa	420
caccagcggc	tggggggcggg	ggcggacctt	gtgaggctca	gttgacccgt	tacttgcaac	480
ctgaaaacaa	atcatgtttt	tgacttaaat	tcttttctct	ggagaaccca	aggggcttgg	540
ggtgggaagc	agtctctcct	tgggattctg	cggccgatgt	gggatagaag	aggtagcatc	600
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caggatctga	gcatgtccct	gggattctga	gctgccaaca	gggccctggg	tagtcacatc	780
ttgtactccc	ctttgctgtc	ccggaggtag	tggcaggagt	tgggccagcc	cccactaagt	840
ggcaggggaa	gactcacgat	tgggaagcta	cctctttggg	aatcttggat	gtggtgatct	900
caagtcccca	caggccacct	ccttctggcc	actcactgct	gggacccagg	cacctccctt	960
ctccatcctc	tctggattgt	cagttaatgtc	ctggaacaga	agcctgtagg	atggccttgg	1020
gcacggagaa	gccttggggt	cagtgtcgtg	cacggatggc	ggcagtgttg	aaccaggag	1080
gctgaacccg	gcccaccag	gaagatgagt	gcatggcaac	cgccctgcctt	cacgtcgctc	1140
cacttggtaa	ccccaaagtc	tgggctgttc	taggtattgc	ttcacgtgcc	ccagcaagcc	1200
cttaacaaga	gggcctggtt	ccctgaagaa	ccaatcccag	gaaggggcct	tgatccctcc	1260
gccttgctga	gagtgaaccc	tcgtctctcc	tcacctcca	tttcatttct	gggaattggg	1320
gcttagtttc	gaaccttttg	caaggctgtt	cttactaatg	cccaagcccc	tttaccctc	1380
tccttatagg	ttacacaggg	gagaccaggg	cctcggcaga	agactgctgc	cacacttccg	1440
aatcattctg	cttgccaaat	aggtcatctt	caccagttga	ctgacccaag	tttaggacca	1500
ttggtatcgt	gtgtttaaaa	aacacatata	aaaaaactct	tgtgaatatt	cttgttatgc	1560
tagagaggaa	ggtacttctc	cctctacggc	tctgcgctgg	ggcctatgg	agtaaagttg	1620
tttactgtcc	tttttctgct	tcctctggaa	atgacaggca	ttactctccc	attggcctcc	1680
cttcccttta	tagaaagacc	aagcaggccc	cactggccaa	gaggtacggt	atttggcagt	1740
ctgagttctc	agtaatttgg	aaagttaagg	agttggttcc	tgtgtcacct	ttcagttagt	1800
gtgggaaagg	aagacttctg	ttttcctgag	atcagtgcag	tctcaggcct	ttggcagggc	1860
tcattgatca	gagctgagac	tggaggggaga	ggcatttcgg	gtagcctagg	agggcgactg	1920
gcggcagcag	aaccgaggaa	ggcaagggtg	tttccccac	gctgtgtcct	gtgttcagg	1980
gcgacacaca	atcctcatgg	gaacaggatc	acccatgcgc	tgcccttgat	gatcaagggt	2040
ggggcttaag	tggataagg	aggcaagttc	tgggttcctt	gccttttcag	agcatgaggt	2100
caggctctgt	atccctcctt	ttcctagctg	atattctaac	tagaagcatt	tgtcaagttc	2160
cctgtgtggc	ccttcccccc	agag				2184

(2) INFORMATION ON SEQ ID NO. 58:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1510 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

agcctgggaa acacagtagg gctccacctc tacaaaaaac acaaaaatta gccaggcatg 60
tggcgtcata gtagaattaa tcaaaagcaa gaaaatggct ggaggagctg tcttgttggc 120
aggacctcct ggaactggca agacagctct ggctctggct attgctcagg agctgggtag 180
taaggtcccc ttctgcccac tgggtggggag tgaagtttac tcaactgaga tcaagaagac 240
agaggtgctg atggagaact tccgcagggc cattgggctg cgaataaagg agaccaagga 300
agtttatgaa ggtgaagtca cagagctaac tccgtgtgag acagagaatc ccatgggagg 360
atatggcaaa accattagcc atgtgatcat aggactcaaa acagccaaag gaaccaaaca 420
gttgaaactg gaccccagca tttttgaaag tttgcagaaa gagcgagtag aagctggaga 480
tgtgatattac attgaagcca acagtggggc cgtgaagagg cagggcagggt gtgataccta 540
tgccacagaa ttcgaccttg aagctgaaga gtatgtcccc ttgccaaaag gggatgtgca 600
caaaaagaaa gaaatcatcc aagatgtgac cttgcatgac ttggatgtgg ctaatgcgcg 660
gccccagggg ggacaagata tcctgtccat gatgggccag ctaatgaagc caaagaagac 720
agaaatcaca gacaaacttc gaggggagat taataagggt gtgaacaagt acatcgacca 780
gggcattgct gagctggctc cgggtgtgct gtttgttgat gaggtccaca tgctggacat 840
tgagtgtctc acctacctgc accgcgcctt ggagtcttct atcgctccca tcgtcatctt 900
tgcattcaac cgaggcaact gtgtcatcag aggcactgag gacatcacat cccctcacgg 960
catccctctt gaccttctgg accgagtgat gataatccgg accatgctgt atactccaca 1020
ggaaatgaaa cagatcatta aaatccgtgc ccagacggaa ggaatcaaca tcagtggaga 1080
ggcactgaac cacctggggg agattggcac caagaccaca ctgaggtaact cagtgcagct 1140
gctgaccccc gccaaacttg ttgctaaaaa caacgggaag gacagcattg agaaagagca 1200
tgtcgaagag atcagtgaac ttttctatga tgccaagtcc tccgccaaaa tcctgggctt 1260
gaccaggcag ggataagtta cattgaagtt gagatggctt gaggggtttt cagcagctaa 1320
gagacttccc caggtgtgcc tggcctgggg tccagcctgt gggcgctttg ccctgggggt 1380
tgggggctgc ctttcccat tcaggcgttg ggttgacgag ttgttcaatt tcagttgttg 1440
gaaagcggtt tttttttgaa gttagtctta agtgtttccc cttggggtttg ttttgaagaa 1500
aacccttcct
1510

```

(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

gagaactcac accatatgtg tcctgttcca gtgcgcgggt ctgtggagag cggggtgcga 60
gcggcggcag caagagggga aaagagctga gcggagacca aagtcagccg ggagacagtg 120
ggtctgtgag agaccgaata gaggggctgg ggccacgagc gccattgaca agcaatgggg 180
aagaaacaga aaaacaagag cgaagacagc accaaggatg acattgatct tgatgccttg 240
gctgcagaaa tagaaggagc tgggtgctgcc aaagaacagg agcctcaaaa gtcaaaaggg 300
aaaaagaaaa aagagaaaaa aaagcaggac tttgatgaag atgatatcct gaaagaactg 360
gaagaattgt ctttgggaagc tcaaggcatc aaagctgaca gagaaactgt tgcagtgaag 420
ccaacagaaa acaatgaaga ggaattcacc tcaaaagata aaaaaagaa aggacagaag 480
ggcaaaaaac agagttttga tgataatgat agcgaagaat tggaagataa agattcaaaa 540
tcaaaaaaga ctgcaaaacc gaaagtggaa atgtactctg ggagttaac aaacttccta 600
aaaaagctaa agggaaaagct caaaaatcaa ataagaagtg ggatgggtca gaggaggatg 660
aggataacag taaaaaaatt aaagagcgtt caagaataaa ttcttctggt gaaagtgggtg 720
atgaatcaga tgaatttttg caatctagaa aaggacagaa aaaaaatcag aaaaacaagc 780
caggtcctaa catagaaagt gggaatgaag atgatgacgc ctccttcaaa attaagacag 840
tggcccaaaa gaaggcagaa aagaaggagc gcgagagaaa aaagcgagat gaagaaaaag 900
cgaaaactgcg gaagctgaaa gaaaaagaag agttagaaac aggtaaaaag gatcagagta 960
aacaaaagga atctcaaagg aaatttgaag aagaaactgt aaaatccaaa gtgactgttg 1020
atactggagt aattcctgcc tctgaagaga aagcagagac tcccacagct gcagaagatg 1080
acaatgaagg agacaaaaag aacgaaagat aagaagaaaa agaaaggagg acaagggagg 1140
aaaagagaac agagaaggaa agaagggcct ggcaaaagcc actgtttc 1188

```

(2) INFORMATION ON SEQ ID NO. 60:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2208 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

gcaggacggc tctgggccct tctgggtga cttcaacggc ttctcccacc tggagctgag 60
aggcctgcac acctttgcac gggacctggg ggagaagatg gcgctggagg tctgttctct 120
ggcacgaggc cccagcggcc tctgtctcta caacgggcag aagacggacg gcaaggggga 180
cttcgtgtcg ctggcactgc gggaccgccc cctggagttc cgctacgacc tgggcaaggg 240
ggcagcggtc atcaggagca gggagccagt caccctggga gcctggacca gggctctact 300
ggagcgaaac ggccgcaagg gtgccttgcg tgtgggagac ggccccctg tgttggggga 360
gtccccgggt ccgcacaccc gtgctgtctc gaaggagccg ctctacgtag ggggagctcc 420
cgacttcagc aagctggccc gtgctgtctc cgtgtcctct ggcttcgacg gtgccatcca 480
gctggtctcc ctcgagggcc gccagctgct gaccccgga cactgtgtgc ggcaggtgga 540
cgtcacgtcc tttgcaggtc acccctgcac ccgggctca ggccaccct gcctcaatgg 600
ggcctcctgc gtcccagggg aggtgccta tgtgtgctg tgtcccggg gattctcagg 660
accgactgc gagaaggggc tgggtggaga gtcagcgggg gacgtggata cttggcctt 720
tgacgggcgg acctttgtcg agtacctcaa cgctgtgacc gagagcgaga aggcactgca 780
gagcaaccac tttgaactga gcctgcgcac tgaggccacg caggggctgg tgctctggag 840
tggcaaggcc acggagcggg cagactatgt ggcactggcc attgtggacg ggcacctgca 900
actgagctac aacctgggct cccagcccgt ggtgctgcgt tccaccgtgc ccgtcaacac 960
caaccgctgg ttgcgggtcg tggcacatag ggagcagagg gaaggttccc tgcaggtggg 1020
caatgaggcc cctgtgaccg gctcctccc gctggcgccc acgcagctgg aactgatgg 1080
agccctgtgg cttgggggccc tgcggagct gcccgaggc ccagcactgc ccaaggccta 1140
cggcacaggc tttgtgggct gcttgcgagg tgtgggtggg ggccggcacc cgctgcacct 1200
gctggaggac gccgtcacca agccagagct gcggccctgc cccaccccat gagctggcac 1260
cagagccccg cgcccgctgt aattattttc tatttttgta aacttgtcgc tttttgatat 1320
gattttcttg cctgagtgtt ggccggaggg actgctggcc cggcctccct tccgtccagg 1380
cagccgtgct gcagacagac ctagtgtgta gggatggaca ggcgaggtgg cagcgtggag 1440
ggctcggcgt ggatggcagc ctcaggacac acaccctgc ctcaaggtgc tgagcccccg 1500
ccttgactgc cgcctgcccc acggtgtccc cgccgggaag cagccccggc tctgaatca 1560
ccctcgctcc gtcaggcggg actcgtgtcc cagagaggaa ggggctgctg aggtctgatg 1620
gggcccttcc tccgggtgac cccacagggc ctttccaagc ccctatttga gctgctcctt 1680
cctgtgtgtg ctctggaccc tgcctcgccc tctgcgcca atactgtgac ttccaaacaa 1740
tgttactgct gggcacagct ctgcgttget cccgtgctgc ctgcccagc ccaggctgct 1800
gaggagcaga ggccagacca gggccgatct ggggtgcctg accctcagct ggccctgccc 1860
agccaccctg gacatgaccg tatccctctg ccacaccca ggccctgcga ggggctatcg 1920
agaggagctc actgtgggat ggggttgacc tctgccgccc gcctgggtat ctgggcctgg 1980
ccatggctgt gttcttcatg tgttgatttt atttgacccc tggagtgggt ggtctcatct 2040
ttccatctc gcctgagagc ggctgagggc tgcctcactg caaaatcctc cccacaaaag 2100
cggtcagtga aaagtcggtc ctttgccta aaaaatgacc aaggggcaa gcaagttttg 2160
tgaacaaagg gtgaaggggg aagttcgaag aggttggagg ggaatttt 2208

```


(2) INFORMATION ON SEQ ID NO. 61:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 283 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

gaaaaggggg agggggagtg acaatctttg cttggggcct atgacttctc cagccccaag 60
gggagatgcc accgggaaat cccccaatgt ccactagggg gcaggaggcc accgttcttc120
gtactccgga gaacctggct ggagagctct ttcttggtca cccttccctc cagctgtatc180
tctgccctgc agataacgtg aaggactgga gcaaggctgt cctggcctat gagcctgtgt240
gggccattgg tactggcaag actgcaacac cccaacaggg aac 283

```

(2) INFORMATION ON SEQ ID NO. 62:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 184 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

aacggaggat gcctaggctt ctggaggcga agaaggacgc ggcaagctgc gaaaagtcac 60
gggtatctgc aagcatgaaa tgatccgtga atatccgaat ggggcaaccc gtgcaggtgal20
agcctgcaca cctgaataaa tcaggggcag acgcagggaa ctgaaacatc ttagtacctg180
cagg                                             184

```

(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1780 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

tccccccccc gggcaacccc cccatcgggc ccccaaagcg ctgggggttac agccttaagc 60
caccaagccc cgcccgacct tcttctatct ttccattctc ctttccaaag ccatggccat 120
gcgctcctgt gtacaggtgc ataaacacat cagtgtgcc a tccctcacat gcatgtcgtt 180
ccccaccct ccttcccagg gcttctcttg gctccagcgt tctcttgga cctctgcag 240
atacagcctg tgctggaccc ccagccaggg tgagggctca ttctgctctg tcttcccac 300
tgctcagtt tccccaaaa gctgctttca cgtccttcta gtagggggcc tcccatgggg 360
gcaaggatcc cctttaggat tcaatctttc ctctttgggc agttttggct ttgagtcccc 420
cagggatcag ggtgagaatg aagaagagct cagtgagcgg aatgacagca gctgggtggg 480
tggtgtgggg agaggctgag gggaaggcag ctctaagact gggagtggag ttcttgagg 540
tgtggggagg ggggcgtgtt ttcaatttag aaaaatctca gccagctcga gccagagag 600
aatgcgaaag aggaagtctg gaaggagcga ggaatggggt ggggtggcagc gggggccgct 660
cagttgctgt cgctcttgct caccagcacg gcgtccgact cctcggtgat ctccagcagc 720
gcgtgcacgt cggggctgct ccgcgcgcgc aggtcgccgg cctccccccg ctccgcccac 780
ctccaccatc tcggtggcct tgagcacttc cacctggccc tcgcggtatc tcttgacgtg 840
gaaggtgaag ggtggcacct tgtagaccgc ggtcttgagg cgcgcgtaca ccacgtggtc 900
gggcgtgaag gatttgcgca acttgctccc cgacgtcttc agtttctcgc gccgtcggc 960
gggcaccagg cgcgtgcccc gcttgctcat gcgcttctcc aggtgtgccc gcgtcttctc 1020
caggttttcc ttggtcttga ggcgcgtctt ctccaggttc tcgcggttac gcaccttggt 1080
cttctccatc ttctccttg agaaggcctt cttgaagtgc tccacgcgcc gcaggccctg 1140
cgcttgatac gctctgcgcg ggactcctca ataacctcct caacctccac cgctcgtcc 1200
gaagaaagct ccagcgccgc tgcgtcctcc tcgggcccgt cgccctcgcc cagctcctcg 1260
ccctccttct ctggcagcgc ctccgactct ttcagcgatt tgctgatgct cagtttgccc 1320
ggcagcttca cttcatcctg gtagatcatg actttaaagt tgcggcgcgc cagcagctcg 1380
gcctcgttga cctccagctt cttgatctgc ccgcctggc gctccaggct gccgcgcacg 1440
gtcttcacgt tgacgtgac cttgcgcacc ttctccagca gcttgctcac cgtattgctc 1500
gtgggtggcg gcgccttgcc cagcttgctc agctcgccct ggatgctctg cactgcgccc 1560
tccatctccg cctgcgcgtc ctccagctgt gcttgagtca gctggatctg gtctacggcc 1620
ccgatgattt tgtccaggag gctcagcacc agcacgccgt tcacctggtc cgacttgatc 1680
agctcttctg agccggcccc cgacggctcc tccgctgcct gagccccagc ggaggaagct 1740
ccggggcctc ggcgatcggg gtaccggggc aagcggccgc 1780

```

(2) INFORMATION ON SEQ ID NO. 64:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1652 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

ctcgagcggc tcgagccgat tcggctcgag cggctcgaga agaagatatg ctagtctgta 60
tttttgcgtg gctattgagg atcaggacaa tgaactaatt accctggaaa taattcatcg 120
ttatgtggaa ttacttgaca agtatttcgg cagtgtctgt gaactagata tcatctttaa 180
ttttgagaag gcttatttta ttttgatga gtttcttttg ggagggaag ttcaggaaac 240
atccaagaaa aatgtcctta aagcaattga gcaggctgat ctactgcagg aggaagctga 300
aaccaccagt agtggttctt gaagaaattg gactgacata actctctctc cttgttgatg 360
acttcttggt gcatttcaca cactgtagat ggtcactccc ttcagtcca tgtagctca 420
tggtgtaaga tgatgtcttg tcagtattac tgttttgcta agccgcttca ttcatgccta 480
cacaattttt ttttaaaagg gaactttagt taattaagtg ataagggact taaatatgaa 540
ttagaatggt gcagaaagag ataccttttc tggatatttt aaagttttaa ggtagtttc 600
tcttaatctg attatgtgca catatgaaaa tggcacatca tatacatgta aaatcaggca 660
gtatacattt attaattact gtatttgaca aaggaaactc tttaaattata atgtgaaacc 720
tggttttatg aaaccaaaga ctagtgcagc atttcagcat atgtaaaaag aaaaaaaaaa 780
gggaattgac atgtcacata tcaaatgaat ggaaactttg ttgaaacttt aaaaagcaaa 840
tttactccaa agacttgat tggaattac ataccttttt tttttttttt aaaggactac 900
agattatttt taatgactaa attggagtga tacttcttac actaaaaatt atttcttagg 960
cattctgaat ctgggatgag aaacaggatt gtttcacaat agtaagcaca taatttttaa1020
ggccaaggca catttgactc ctgagatgaa ttttttgagg tcataatcaa atacttagtt1080
gtttttgatg ccccaaaata aagtgagaat ggtaatttgc caggaattct tcataacagt1140
atcttacaaa aaacgtgttg ctctcttcac agtattatgt gtaaagtcac tgtttaaagc1200
acgaatgttc cctctggggt acttgtaaaa gctaaattta ttttgcttcc ctccacttag1260
aagtgtgca cactttacag cagcttcctt tctttccatg gcactgccta gttaacagaa1320
gtcttataaa aatttaaaaa gacacatttc ttacaaaaaa gagttgaatg aggtaaaatg1380
gcattagatg gctctatatt ttttaaagct atgtaattgt tcagcgtcac ttttctaagt1440
acttatacat atctaaacat gtcttcattg tttatatttt cacttatata tgctgggctg1500
gattaagctt tgttgatgatt gtgaccaaca ttcaggccac gtgagcactg tcttatcaca1560
tcgccaatta gttgtaataa acgttcaacg tacaacaaaa aaaaagggcg cagcttcctt1620
ggggggaatt actggaagcg gggtaagcg ga
1652

```

(2) INFORMATION ON SEQ ID NO. 65:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1085 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```

gctccctggc ctccctctca gacagcttgg ggggtgtctgt catggccacc gaccaggact 60
cctactccac cagcagcacg gaggaggagc tggagcagtt cagcagcccc agcgtgaaga 120
agaagccctc catgatcctg ggcaaggctc ggcaccggct gagctttgcc agtttcagca 180
gcatgtttcca cgctttcctc tccaacaacc gcaagctgta caagaagggtg gtggagctgg 240
cgcaggacaa gggctcgtac tttggcagcc tgggtgcagga ctacaagggtg tacagcctgg 300
agatgatggc gcgccagacc tccagcacgg agatgctgca ggagattcgc accatgatga 360
cccagctcaa gagctacctg ctgcagagca ccgagctcaa ggccctgggtg gaccccgccc 420
tgcactccga ggaggagctc gaagcaattg tagagtctgc cttgtacaaa tgtgtcctga 480
agccctgaa ggaagccatc aactcatgcc tgcatacagat ccacagcaag gatggttgc 540
tgcagcagct caaggagaac cagttagtga tctggccac caccaccact gacctagggtg 600
tgaccaccag cgtgccggag gtgcccatga tggagaagat cctgcagaag ttcaccagca 660
tgcacaaggc ctactcacct gagaagaaga tctccatcct gctcaagacc tgcaaactca 720
tctacgactc catggccctc ggcaaccag ggaagcccta tggggcggtat gacttctctgc 780
ctgtgctcat gtatgtgctg gcccgcagca acctcacgga gatgcttctc aatgtggagt 840
acatgatgga gctcatggac cccgccctgc agctggggga gggttcctac tatctgacca 900
ccacctacgg ggccctggag cacatcaaga gctacgacaa gatcacggtg acccggcagc 960
tgagtgtgga ggtgcaggac tccatccacc gctgggagcg ccggcgctact ctcaacaagg1020
ccggggcctc ccgctcctcc gtacagccac ttcactctgcg tgcgtacct ggagcccag1080
cagca
1085

```

(2) INFORMATION ON SEQ ID NO. 66:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1393 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

gggcagggga gggagttgac gggctgacac aggaaactcc cctgaaacct gtttctcagc 60
ttcccggccc agctggggca cccactggaa ggagaggcca ggcggaagac cctgggtccg 120
tcatggcctc tgccctgagg ccaccccggtg tccccaagcc taagggtgtc ctgccttcac 180
actactatga gagctttcta gagaagaagg ggccctgtga cggggattac aagaagttct 240
gggcaggcct gcagggtctc accatttatt tctacaatag caatcgggac ttccagcacg 300
tggagaagct caacttgga gcatTTgaga aactcacaga tgagattccc tggggaagct 360
cacgtgaccc tggcaccac ttcagcctga ttctccgaa tcaggagatc aagttcaagg 420
tagagacctt ggagtgtcgg gaaatgtgga aaggcttcat cttaacggtg gtggagctcc 480
gtgtcccga cgaactgacc ctgcttcctg ggcacctata catgatgtct gaagtcttgg 540
ccaaagagga ggcgcgccgt gcactggaga caccctcgtg ctTcctgaag gtgagccggc 600
tggaggcaca actgctcctg gagcgctacc ccgagtgcgg gaacctgctg ctgcggccca 660
gcggggacgg cgccgacggt gtccggtcacc acgcggcaga tgcacaacgg gacgcacgtg 720
gtccggcatt acaagggtgaa gcgggagggg cccaagtac gtgatcgatg tggaaacagcc 780
gttctcttgc acctccctgg acgccgtggt caactatttc gtgtcgcata ccaaaaaggc 840
gctggtgcca ttctgttag acgaggacta cgagaagggt ctaggctacg tggaaGCCga 900
taaggagaat ggcgagaatg tgtgggtggc gccctccgct ccgggcccag gtcctgcacc 960
ctgcacaggt ggccccaagc cgctgtcacc tgcgtctagc caggacaagc tgccccact1020
gccccacta ccgaaccagg aagagaacta cgtgaccctt attggagatg gccagctgt1080
tgactatgag aaccaagatg tggtctctc tagttggcca gtcattctga agccaaaga1140
gttgccaaag cctcctgcca agcttccaaa gccaccggtt ggaccaagc cagagcccaa1200
agtctttaat ggtggcttgg gcagggaagc tgccagttca gtttcagccc agcctcttct1260
ttccccacag gccgggctgg gcagacatgg acggcagagt tacagaagaa gctgggagaa1320
gaggcggggc actggtagca tggtttcggg cacaccaggg accagcgggt tagttccagg1380
gcggggccagg tgg
1393

```

(2) INFORMATION ON SEQ ID NO. 67:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

ggcacgagga agttaagatc atacatgagg atgtgctggt aacctgcaag aagcaatcat 60
gctgcggtcc ggtgtgacct cccaaggcat taccctggg agtccctggt gctgcacccc 120
aaccaggga gagctcatcg tgggtgacca gagcggggct atccacatct gggacttgaa 180
aacagaccac aacgagcagc tgatccctga gcccagggtc tccatcacgt ccgcccacat 240
cgatcccagc gccagctaca tggcagctgt caatagcacc ggaaactgct atgtctggaa 300
tctgacgggg ggcatgggtg acgaggtgac ccagctcatc cccaagacta agatccctgc 360
ccacacgcgc tacgccctgc agtgtcgctt cagccccgac tccacgtcc tcgccacctg 420
ctcggtgat cagacgtgca agatctggag gacgtccaac ttctccctga tgacggagct 480

gagcatcaag agcggcaacc ccggggagtc ctcccgaggc tggatgtggg gctgcgcctt 540
ctcgggggac tccagtaga tgcactgc ttctcgagc aacctggccc ggctctggtg 600
tgtggagact ggagagatca agagagagta tggcgccac cagaaggctg ttgtctgcct 660
ggccttcaat gacagtgtgc tgggctagcc tgtgacctc cgggactgcc tgggtgcagg 720
ggtggcagct ggagggaccc atgcagcacc caggctcagag cagaccctcc cctgccggcc 780
tgcgccactg gacctgatgg cccctgtgg cgccttgacc tgcgtggcca ggctgccctg 840
ggactctcag ccccgagttg cttatccaga tgtgacagag ctgcaccaa gccaggctgc 900
acactcctgg actgggctag cctgcaactgc ctgggaaagt cggccgaggg cccaaagctg 960
ctgaggggtc tgaggctggt gcccaccccc aagctagtgt gttctctgcc cctccctgcc 1020
cgcgtttcag ggcctcggtc catagagaac accaccacca tggccagggtg gaagggtttal 1080
ttagtccctg ccagcagctg tccctccctg tgcagggtggc ctggccagcc cactggattg 1140
gggacgggcc aggtctgggcc aggtcggggg ctgagctctg gaggttaataa aagcagaccg 1200
acacgcagat gttgctcggg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1248

```

(2) INFORMATION ON SEQ ID NO. 68:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

ctcgtgcaat ttcgggcagg gagtgtcaag cctgttgtct taacattttg tataaaaaag 60
aacaacagaa attatctgtc atttgagaag tggcttgaca atcatttgag ctttgaaagc 120
agtcactgtg gtgtaatatg aatgctgtcc tagtggtcat agtaccaagg gcacgtgtct 180
ccccttggtg taactgattt ccttttttagt cctctactgc taaataagtt aattttgcat 240
tttgacagaa gaaacattga ttgctaaatc tttttgctgc tgtgttttgg tgttttcatg 300
tttacttggt ttatattgat ctgttttaag tatgagaggc ttatagtgcc ctccattgta 360
aatccatagt catcttttta agcttattgt gtttaagaaa gtagctatgt gttaaacaga 420
ggtgatggca gcccttccct agcacactgg tggagagac cccttaagaa cctgacccca 480
gtgaatgaag ctgatgcaca gggagcacca aaggaccttc gtttaagtgt aattgtcctg 540
gcctctcagc catgaccgtt atgaggaaat atccccatt cgaacttaac agatgcctcc 600
tctccaaaga gaattaaaat cgtagcttgt acagatcaag agaataact gggcagaatg 660
aagtatgttt gtttattttt ctttaaaaat aaaggatttt ggaactctgg agagtaagaa 720
tatagtatag agtttgcttc aacacatgtg agggccaaat aacctgctag ctaggcagta 780
ataaactctg ttacagaaga gaaaaagggc cgggcacagt ggcttattcc tgtaatccca 840
acactgtgga aggccgaggc aggaggatca cttgagtcca ggagtttgaa acctacctag 900
gcaacatggt gaaaccttgt ctctaccaa ataaaaatta gctgggcatg gtggcacgtg 960
cctgtgtgtc cagctacttg ggaggctgag gtgggagcct gggaggtcaa ggctgcagtg 1020
agccatgatc atgccactgc actccatcct gggtgacagc aagatcttgt ctcaaaaaaa 1080
aaaaaaaaa aagtcgacc 1099

```

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 774 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

tttatggagc ctgtactatg taccagatgc agactgtgct agcggttggg gatacagtga 60
tgacttggtc tgcctctagg tggcaggag ccattttggg ttttcgaaca gaaaagtga120
ataatgaatg ctgagttctt aggaagatta atccaggagt agtctccagg atgtactgga180
aggagagaag ctgaaaccag ggaggctgct gtgtttgcag ttggctgccc agtgctacct240
ctgcagagac aatcaatgtc ctgaaggtag ctggtatgtc tgtgtgcact gacacgagcc300
ttcctaccaa gccccagggg ctccatgctg gagaatgcac gtagggctag ggtgagca360
aacttcactt caggagagca aggaacagtg tggctcttcc atttttcagt tctgtaagca420
catcaccctt ttctcctccc cttgagctgt gttctctgac agctgtttgt tggtaaagcc480
agcagccctt aaagcacgtc ccagccttgt ctctctgtg ctttcccca ccactgctgc540
tgacgcctc atttgctggg ccactttagt ggtggaacca ttagaggctg agtgacttaa600
aggagattga gtctgtctcg accccgagag agagtgggat ggatggatgc atcgtctcat660
ttagaaagtg ttgcctctga ctctaacaca ctcttctctc tttctttacc gccctccctg720
tgtgcgtccc tggggggggcg tgggctaaac cccttccgtc cccctttctc cttc 774

```

(2) INFORMATION ON SEQ ID NO. 70:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 426 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

tagctccagt ctcagctgta tcattttcta actgattttt acaataaaaa tgagagtaaa 60
aatcagttac tctttctaga cattaattag cacattttacg ttaagactct aagtagtata120
aaatgtaaat tgctgctacc ctactaagtt actgtcagta aatactgtgt gcagtaaatg180
ttgagtatgg attaatgaa ggatacctct acaattattt cctttagtca aggttgttagc240
taagaattgg gcttctgaca tacattcttt ttaatctttt tcgtattggg ttttatagca300
ctaaacctaa tttctaacat atttttacac ctgaaatcta cattctaata taaaggtttt360
ttttttaaac gttcctaaaa tttcaggccc tcagcaggca gtttttgtcc cagttttctt420
caacag

```

(2) INFORMATION ON SEQ ID NO. 71:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1417 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```

gccaaccttc cctcccccaa ccctggggcc gccccagggt tcctgcgcac tgcctgttcc 60
tcctgggtgt cactggcagc cctgtccttc ctagagggac tggaacctaa ttctcctgag 120
gctgaggag ggtggagggt ctcaaggcaa cgctggcccc acgacggagt gccaggagca 180
ctaacagtac ctttagcttg ctttctctct ccctcctttt tattttcaag ttctttttta 240
tttctccttg cgtaacaacc ttcttccctt ctgcaccact gcccgtaacc ttacccgccc 300
cgccacctcc ttgctacccc actcttgaaa ccacagctgt tggcagggtc cccagctcat 360
gccagcctca tctcctttct tgctagcccc caaagggcct ccaggcaaca tggggggccc 420
agtcagagag ccggcactct cagttgccct ctggttgagt tggggggcag ctctgggggc 480
cgtggcttgt gccatggctc tgctgaccca acaacagag ctgcagagcc tcaggagaga 540
ggtgagccgg ctgcagggga caggaggccc ctcccagaat ggggaagggt atccctggca 600
gagtctcccg gagcagagtt ccgatgccct ggaagcctgg gagagtgggg agagatcccg 660
gaaaaggaga gcagtgtca cccaaaaaca gaagaatgac tccgatgtga cagaggtgat 720
gtggcaacca gctcttaggc gtgggagagg cctacaggcc caaggatatg gtgtccgaat 780
ccaggatgct ggagtttata tgctgtatag ccaggctctg tttcaagacg tgactttcac 840

catgggtcag gtggtgtctc gagaaggcca aggaaggcag gagactctat tccgatgtat 900
aagaagtatg cctcccacc cggaccgggc ctacaacagc tgctatagcg cagggtgtctt 960
ccatttacac caaggggata ttctgagtgt cataattccc cgggcaaggg cgaaacttaa1020
cctctctcca catggaacct tcctgggggt tgtgaaactg tgattgtgtt ataaaaagt1080
gctcccagct tggaagacca ggggtgggtac atactggaga cagccaagag ctgagtatat1140
aaaggagagg gaatgtgcag gaacagagga gtcttctctg gtttggtctc ccgttcctca1200
cttttccctt ttcatcccca cccctagac ttgatttta cggatatctt gcttctgttc1260
cccatggagc tccgaattct tgctgtgtg tagatgagg gcgggggacg ggcgccaggc1320
attgttcaga cctggtcggg gccactgga agcatccaga acagcaccac catctaacgg1380
ccgctcgagg gaagcaccgg gcggtttggg cgaagtc 1417

```

(2) INFORMATION ON SEQ ID NO. 72:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 691 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

ctgccttccg gtgcgtcggt tacgccagtt tgaaccaaag acgccaag ttgaggccga 60
gttccagagc atgggggtctc ggttggtccca gccttttgag tcctatatca ctgcgcctcc120
cggtaccgcc gccgcgcccc ccaaacctgc gccccagct acaccggag cgccgacctc180
cccagcagaa caccgcctgt tgaagacctg ctggagctgt cgcgtgcttt ctgggttggg240
gctgatgggg gcgggcgggt acgtgtactg ggtggcacgg aagcccatga agatgggata300
cccccgagt ccatggacca ttacgcagat ggtcatcggc ctacgcattg ccacctgggg360
tatcgttgtc atggcagacc ccaaaggga ggcctaccgc gttgtttgaa agtaccacca420
gtgaatctgt cttctgtctc tgtccctttc cccgtgacac acagagcagg catggaattt480
aatgggtggt ctggacagac acttgtagat ggacagacat cactactgtg gatactacaa540
gactgaaaag aaaatcgtag gttgtcattc tctggctatg gagtgtttgt ggccttcaca600
gatttcacag gaaccaataa atccctcaga gaagtaaaaa aaaaaaaaaa aaaaaaaaaa660
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a
691

```

(2) INFORMATION ON SEQ ID NO. 73:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1705 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

gattcggcat gaggacagag ccctttttga aaataaattg gcattggagt gttttaccct 60
ctagctgttt tacttagaat gtaacatatg ctgcctaccc acctcaaat gtctgtactg 120
caagagggcc ctgggectct gctttccata ttcaagtttg gccagagttg tagtcccaaa 180
gaagagcatg ggtggcagat ggtagggaat tgaactggcc tgtgcaatgg gcatggagca 240
caaggggtca cagcatgcct cgtgccttac cgtggcagta cggagacagt ccagaacatg 300
gtcttcttgc cacggggtgt tgttgtctct ggtggtgctg catgtctgtg gctcaccttt 360
attcttgaaa ctgaggttta cctggatctg gctactgagg ctagagccca cagcagaatg 420
gggttgggcc tgtggccccc caaactaggg ggtgtgggtt catcacagtg ttgccttttg 480
tctcctaaag ataggatct acttttgaag ggaattgttc ctcccaaata aatttgcttt 540
accttgggcc tttcttttgt gccagtattc aagtgggata gctctgagca gggtcacatt 600
tgGCCAAACC tgacactgtc ttgctgcatt ctcccttggc aaacatcagg gtcagaattc 660
aggatagccc ttcttagggc actggacttt ctggcatggg ggctgtgttt gcacaagtta 720
tttcatgtt acctggagag tgtccagagg ctgctctgag gctgagggtg gttccccctt 780
gcctggttcc agctgtcaga gggataccat cctagggtct gggaatccaa ggccacgaga 840
ctccttggtt tgtggtccga gatcctgtac taaggagggt ctggccagag gaacagacca 900
gcttttgcac aatgaagcgc aagggaacaa gtggtttgcc tgggtgccta cctgtcctga 960
acctggtcct gtgggccatt gaaaagttag atctgtgate tctggggttt ttgtggcttt1020
gttcaatgct tccactctag ggcaggcaga gcagtctata ctctcccaag cctgcttgac1080
ctccaagtag agctgataca gagatctgtg aatattgtga tagaaattct ttggtattca1140
tacatttcag ctgcaagtca gcaatttccc aggtaccatg taagctataa aacagtcatt1200
cttaaagaca gaggatagct gtgactcatg ggatcatgag gtccatggct ggttgaggt1260
tccctttttc ctccctcagg ttttgtctct tctgtgttg tccccagcaa gggagagact1320
gtggggtgga ttgggagaac agattaggag tatagcaaat gaaccagaa tggaacagt1380
gggagctaac tgtgaatgag gagagtacct gctgcaggac ctggaggtca ggtgtgaat1440
ctgtattggc acagggaata aatatcctgg cgtctggagc cttcacctct ccgtcaagtc1500
cttctgtga tactgccatg gcacaggatc tgagttgcag ctctgcaccc taaatcacac1560
cctgggcatt gtctgggctg cagggtgcc aggttctgta cttgtgtcca gctgtggccc1620
tggtgcccgg aaactgggag ggggttcttg tgcccagaat gtagcctgta acgcttgggc1680
gccttttaaa gccccccctg gggcc

```

1705

(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1516 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

gtttattcctt agtagttgga actaatgtag tctgactaaa atacacatgg gtgtctgctc 60
tgtgatgttt aaacttatct gttttgtttg gttttcattt caggaagcag aagtgcgaagc 120
aaagcagcaa gcatgaacct taagcactgt gctttaagca tcctgaaaaa tgagtctcca 180
ttgcttttat aaaatagcag aattagcttt gcttcaaaag aaataggctt aatgttgaaa 240
taatagatta gttgggtttt cacatgcaaa cattcaaaat gaatacaaaa ttaaaatttg 300
aacattatgg tgattatggt gaggagaatg ggatattaac ataaaattat attaataagt 360
agatatcgta gaaatagtgt tgttacctgc caagccatcc tgtatacacc aatgatttta 420
caaagaaaac acccttccct ccttctgcc aacttaagt tatctgcagc 480
tctacattaa aaaggagaaa gagaaataac ctgtctctca ttcttaagt gcctcattaa 540
ttttcatgaa caagaatatg tacctttttg atgctatatt actgcgatta aaaagttctt 600
gcaggtaatg tttatgatat gttaaactgt gtaatttctt atcgtaatta taacattccc 660
attcttttgt agatgaaact tctacatatt gaaccacaga ttttctgagc ttctaaatgt 720
agcctttcat tgcacatttc agtgatcaga atagatatcc ttttacacgc acaaaagcaa 780
tagattcatt cagtggacaa gttccttggt taactacaca gctatgatgg aatgatatat 840
ccaagttcct tgcctcagtg aaatatgcat atgtatatca tgaaagtggg atgccaagta 900
agcttaaaat ggcattctct agcaaagaga ttagactttt aaataactct tataaaacag 960
gttggcgatc atttcccaag attggtttcc cttgagtttt tgctaaaaca aatcttagta 1020
gttttgcccg tttaaaacaa ctcaaatcg taaatgctac tattcctaag atatcttacc 1080
tttttatttc agtttagcca tgtattgtat gagtgtatta gtctaagcag tgagaatctt 1140
ttctatgcct ctattccagc aaaaagtaga agtatcaa ataaaaggga acttttaaaa 1200
tattaagcct gaagacttct aaaaagacaa gaaacatggc ctataataacc aacatagatt 1260
tacatagtaa gtttcacact accttattac caaaagcaaa cacctcttac tttaaactac 1320
attatcatgt atatctattg tatgctggtc tttacttttt gccaaaatca acatataatg 1380
aagagatgcc tttgtttcat gagattcaaa cttgatgcta tgcttttaaa taaactcagt 1440
acttttagaa acataaaaaa aaaaaaaaaa aggcgacccc ccgagtagtg ggcccgcgcc 1500
cggggatttt tccggg                                     1516

```

(2) INFORMATION ON SEQ ID NO. 75:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1490 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

gaataaaggg ctggccagac ccagtggcgt cctttcccag acctttcttg gcacaaagcc 60
tttgctgcct ggcttgagg ccctgcccgc tacattctct ggacccact atgtgcctgg 120
caaagggcta gtgccttgag gaaactgagg tagctgggtt ggtccccttc caggaattca 180
gagtctggtg gcaggggcat gggaaataga cagatgtaat tctatagcct gggcctggca 240
ccctccacct ccacgcccc ccagcattgc cttacgcctc ccttgcccca cgtagatgg 300
tttcttcogg ttttgcactc tggctgcccc ttggagtctc ctggggagct gtaatatctc 360
tttgagagatt cagattgagc tggcttaggt tgtggcccag gcattgggca ttttgaagc 420
ccccaggtgt tttcagcttg cagccaggcc gagagagagc ccctgagtca gatcccatg 480
gttttaggcac acctagcggg aggggtggct cctggacccc accgtggttg gagagctgag 540
catgtgtgtg gcttttagtg ggtctgttag ttatgggggt ctgggcactg gagctgcagg 600
acacttggga tcccaggtca gaaaggcca gatgagcaac taggaaagac ttgggggcca 660
gggcgagtg gggtcacctg aactcttgt gagggccctt ctagtgcctg ctcacaccgg 720
aatttcattc actccaagaa gccatcaggg gtaagatacc ttcctttaa cgtcactaag 780
aaagaagagg cctgccggtg acacagtaag atgccattga tctaaagatg cgtcttgatt 840
tcagaaaggt ccggaagtgg aaagcaggtt tcagggtgc tgaggtacag ggttctcctg 900
taggccccag ggatggtctc aggggtgctg agtgcggtgc tggtaaattg atggagccca 960
ggggcgccctc ctgccagtgt cctccaggca ctcaaaccta gcccttctga agccgacctc 1020
acgtgacctc acagccccctc ctgaaggcgc ctactgatg acggtgggtg gaataacagc 1080
ccccagagat gtccaggttt ggaaccccag gacgtgggaa agtgttacct tgcgtggcaa 1140
aagggacctg gcgcctgtgc ttcagttcag gatttcgtgg tggggagatg accgtggatg 1200
gttgaggtgg gccctgagta atcatggggg cccttataag ggaaggggag tcacgagggg 1260
ctgcgcatga agcaaggaag cttctggctg tgaagatggc aagaaggcct ggggccaggc 1320
gatgaggtgg ccctggagg agctggaaaa ggcattggat tctgccccag agcctccgtg 1380
gagaaacaaa gccgcactga caagacttca gcctggtgaa aaccattttg gactcctgac 1440
ctctagaact gtaagataat aaattggtgt ggttttcaac ctctcaaatg 1490

```

(2) INFORMATION ON SEQ ID NO. 76:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2513 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```

ctcgagccga ttcggtttca gcagaaagtg atggaaaaag aaactgaaaa ggcattttct 60
gaaatcgaag atgctgcatt cctggccccg gagaaagcga aacaagatgc tgaatattat 120
gctgcacaca aatatgccac ctcaaacaag cacaagttga ccccggaata tctggagctc 180
aaaaagtacc aggccattgc ttctaacagt aagatctatt ttggcagcaa catccctaac 240
atgttcgtgg actcctcatg tgctttgaaa tattcagata ttaggactgg aagagaaagc 300
tactccccct ctaaggaggc tcttgaaccc tctggagaga acgtcatcca aaacaaagag 360
agcacagggt gatgcaagag gtggaaatgt tctccatata aagatgtggc ccaaggggtt 420
aagtgggaac aatcattata cggactcttc agatttacag agaacttaca cttcatctgt 480
tccacctctc ctgcatagat cctgggtgct ccactgattg gaggatagag ccagctgtct 540
gacacacaaa tggctctttc agccacagtc ttatcaagta tcctatatgt attcctttct 600
aaactgctac tcatgaatga ggaaagtctg atgctaagat actgcctgca ctggaatgtt 660
aaacactaaa tatataacaa gctgtgtttt cctaagctga gatctgttga ataatgttta 720
cattcgtccc ccggggaaat gtatgctcag ccaccattca agagatgact gagaaggaga 780
tggttaagttc aagaagactg attgcacctg ggagccaggc cctttctttg ggatccagtc 840
ccagccttca tccatgtgat taagatccag gccgctgaag ttcccagga aatgatcttc 900
cacttgagca accttttact tgatacagatt tgcaccttct tgttttcctg cagtcagggt 960
ggtggcctgc agggacctga gctttgctac ccaaccagat tcctcataga gattcctaatt 1020
cactagtttc ttgtattcat aaactcagag atacagaggg cttgggttga agttggggtg 1080
agatgaaacc tttgctctga gccaaagctc tggggccttg cattccctgc attgggttga 1140
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acctccttgt. atgttacctt tcagctctgg ccaagagtgg gacagggttt taaccacaaa 1260
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gtttttattt ttaaaactgg atctggggta tattcatttg ccccatcacc tctgtctaaa 1380
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cccaggagat caggattcca ctgacgtcct gggcagccag tgaatttaat tttccatgag 1620
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agaaatcttt cagctgtcag gcctgtcagt ctcatgacag tttgttggtt gtgcaaaca 1860
ctttattttg gaaaggaaag cccagatttg aatgggtctt tcccctgggc cttatcctat 1920
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cccaaagtg atggccctgg aggcggggct gaggaacagg gaaatgccgc tgtgaagtct 2220
taaagcactt ctgcttaaac tcccatgtgt gaggagtgtg cctccctgtg ccctctcagc 2280
tctgaggctg gccgtctttc ggggtgttcc ttttgcaaaa tatacactgt aatcttgagt 2340
ctaaatttat atgttgaaat gctacctttt ttaaaataag aaactaaata aaattatttt 2400
actatcaaaa aaaaagaaag gggagggaag ggggcggagg gggtaggagg gggggggggg 2460
gagggggggg aggggaatgt ctcgagaggg ggggggtggg ggcgccgtcg agc 2513

```


(2) INFORMATION ON SEQ ID NO. 77:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```

accgacggcc gccccttttc gtcttttttt tttttacatt tcaaatatat tttattactt 60
tccatcttag aaagaatatg aaacctgcat gcaatgctaa tggtttctga catgtacata 120
gcatataaca cagcagtaca atgcggcata tactgggggg cagtgtgtgg agggggcggt 180
cttaagggtta tatgtacaga ggaaagggcg catggtcac ttagctttcg aaaggaggact 240
gcactgttta acattgaaga attacatggg gaatcacaaa tatattgctt tagtactgca 300
tgttctgttg tggtagggga aagaaacatg ctttgaagg tttcccttgt caacagaatg 360
tgtgtctgta gctgtgtatt gcgcatgtat tcatatattt ttaagttttc tcctaagggt 420
tttgctgaca gtgttgggaa cctcacatgc ttctgaagca ttaaattattg aacctgtgaa 480
cctttcagaa atcctcaggt tgggaaagac cccacacctt ctttaaggat catttgtctc 540
gccatcacag gatcttgga atgtttccta ggggtgtgta aaattaacca ggggggaatg 600
aagcacattt ttctggcaac caaacttgag ttccctcagag aacagatgca gagagacctg 660
ctctgcttg cccggctaca ggggccactg tggagtcaca ctgaggctgt gaccggccat 720
aagcccagga gatcccggtg cagctgtgcc gagggccag gacctctaag cggaagcttc 780
ccaagctagg aatggagcaa cactgcaatg aaatgtgtcc accaagctca ttgttcctcc 840
cgggcgctta taaagctcag atgtatagtg acgtatggac aaatacaaaa aaaaaaaaaa 900
aaaaaaaaa aaaaaaagcc tttctttctc acaggcataa gacacaaatt atatattgtt 960
atgaagcact ttttaccac ggtcagtttt tacattttat agctgcgtgc gaaaggcttc1020
cagatgggag acccatctct cttgtgtctc agacttcac acaggctgct ttttatcaaa1080
aaggggaaaa ctcatgcctt tcctttttta aaaatgcttt tttgtatttg tccatacgtc1140
actatacatc tgagctttat aagcgccccg gaggaacaat gagcttggtg gacacatttc1200
attgcagtgt tgctccattc cttagcttggg aagcttcgc ttagaggctc tggcgctc1260
gcacagctgc cacgggctct cctgggctta tggccggtca cagcctcagt gtgactccac1320
agtggccctt gttagcgggc aagcaggagc aggtctctct gcatctgttc tctgaggaac1380
tcaagtttgg ttgccagaaa aatgtgcttc attccccctt gggttaatttt tacacacctt1440
aggaacattt tccaagatcc tgtgatggcg agacaaatga tccttaaaga aggtgtgggg1500
tctttcccaa cctgaggatt tctgaaaggt tcacagggtc aatattttaat gcttcagaag1560
catgtgaggt tcccaacact gtcagcaaaa acctaggag aaaacttaaa aatatatga1620
tacatgcgca atacacagct acagacacac attctgttga caagggaaaa ccttcaaagc1680
atgtttcttt ccctcaccac aacagaacat gcagtactaa agcaatatat ttgtgattcc1740
ccatgtaatt cttcaatgtt aaacagtgc gtcctctttc gaaagctaag atgaccatgc1800
gccctttcct ctgtacatat acccttaaga acgccccctc cacacactgc ccccgtagt1860
tacgcaggca ttggtaccgg ctggtgttaa aatggctatg ggacatggc aggaaccat1920
ttaggcattg gcattgaggg ttccataatc cgtttctaag ga 1962

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(2) INFORMATION ON SEQ ID NO. 78:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 788 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```

cgttgcccc  gccgcgggcg  cgagatggat  tccgggtgct  ggttggtcgg  cggcgagttc  60
gaggactcgg  tggttcgagga  gaggcgggag  cggcggtcag  gaccgcccgc  gtcctactgc  120
gccaaagctct  gcgagccgca  gtggttttat  gaagaaacag  aaagcagtga  tgatgttgaa  180
gtgctgactc  tcaagaaatt  caaaggagac  ctggcctaca  gacgacaaga  gtatcagaaa  240
gcactgcagg  agtattccag  tatctctgaa  aaattgtcat  caaccaattt  tgccatgaaa  300
agggatgtcc  aggaaggtca  ggctcgggtg  ctggctcacc  tgggtaggca  tatggaggcg  360
ctggagattg  ctgcaaactt  ggaaaataaa  gcaaccaaca  cagaccattt  aaccacggta  420
ctctacctcc  agcttgctat  ttgttcaagt  ttgcagaact  tggagaaaac  aattttctgc  480
ctgcagaaac  tgatttcttt  gcatcctttt  aatccttgga  actggggcaa  attggcagag  540
gcttacctga  atctggggcc  agctctttca  gcagcacttg  cgtcatctca  gaaacagcac  600
agtttcacct  caagtgacaa  aactatcaaa  tccttctttc  cacactcagg  aaaagactgt  660
cttttggtgt  ttcttgaaac  cttgcctgag  agctctttaa  ttttctgtgg  aagggatacg  720
aggaatggca  ggaaaattgg  gaagttttgc  aaatgtgcca  acctggttgg  agaaaggggg  780
acaggttt

```

(2) INFORMATION ON SEQ ID NO. 79:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 299 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```
aacctccctc gaggaattg atcttcagcc ctcccaacctc acaatctaca cagcagcctt 60
gaaggaaaag acgccagact tcagacgtct ctctcctcgc gtctcggaga ccgcggactc120
ccgtaaggtc gcccggtggc cccgatttgt aatgcgggac aaccccgggc gcgggggtga180
tcataggggt ctccaggcgc cggggtggat gaaggagggt cggggatggg gggttttgta240
aagggggctg tagaaggcgg aaggaaggat gaaatttggg aggggggggg gggggtcac 299
```

(2) INFORMATION ON SEQ ID NO. 80:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2263 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

attacgacaa ctcttctaca tgtaagaaag gaaagggtatt ccctgggaag atttcagtga 60
cagtatcaga aacatttgac ccagaagaga aacattccat ggcctatcaa gacttgcata 120
gtgaaattac tagcttggtt aaagatgtat ttggcacatc tgtttatgga cagactgtaa 180
ttcttactgt aagcacatct ctgtcaccaa gatctgaaat gcgtgctgat gacaagtttg 240
ttaatgtaac aatagtaaca attttggcag aaaccacaag tgacaatgag aagactgtga 300
ctgagaaaaa taataaagca attagaagta gctcaagcaa ctttctaaac tatgatttga 360
cccttcggtg tgattattat ggctgtaacc agactgcgga tgactgcctc aatggtttag 420
catgcgattg caaatctgac ctgcaaaggc ctaaccacaca gagccctttc tgcgttgctt 480
ccagtctcaa gtgtcctgat gcctgcaacg cacagcacia gcaatgctta ataaagaaga 540
gtggtggggc ccctgagtgt gcgtgctgct ccggctacca ggaagatgct aatgggaact 600
gccaaaagtg tgcatttggt tacagtggac tcgactgtaa ggacaaattt cagctgatcc 660
tcactattgt gggcaccatc gctggcattg tcattctcag catgataatt gcattgattg 720
tcacagcaag atcaaaataa aaaacgaagc atattgaaga agagaacttg attgacgaag 780
actttcaaaa tctaaaactg cggctcgacag gcttcaccaa tcttgagca gaagggagcg 840
tctttcctaa ggtcaggata acggcctcca gagacagcca gatgcaaaat ccctattcaa 900
gacacagcag catgccccgc cctgactatt agaatacata gaatgtggaa cccgccatgg 960
cccccaacca atgtacaagc tattatttag agtgtttaga aagactgatg gagaagtga 1020
caccagtaaa gatctggcct ccgggggtttt tcttccatct gacatctgcc agcctctctg 1080
aatggaagtt gtgaatgttt gcaacgaatc cagctcactt gctaaataag aatctatgac 1140
attaaatgta gtagatgcta ttagcgcttg tcagagaggt gggttttctt aatcagtaca 1200
aagtaactgag acaatggtta gggttgtttt cttaattctt ttcttggtag ggcaacaaga 1260
accatttcca atctagagga aagctcccca gcattgcttg ctctgggca aacattgctc 1320
ttgagttaag tgacctaat cccctgggag acatacgcat caactgtgga ggtccgaggg 1380
gatgagaagg gatacccacc acctttcaag ggtcacaagc tcaactctctg acaagtcaga 1440
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ggagggctgc ctgggaatcc aggaactttt tgatgcta atagaaggcct ggactaaaaa 1620
tgteccactat ggggtgcact ctacagtttt tgaaatgcta ggaggcagaa ggggcagaga 1680
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ttagagagga ggcacctggg atccaccttc ttcttaggt cccctctctc atcagcaaag 1800
gagcacttct ctaatcatgc cctcccgaag actggctggg agaaggttta aaaacaaaaa 1860
atccaggagt aagagcctta ggtcagtttg aaattggaga caaactgtct ggcaaagggt 1920

gcgagagggg gcttgtgctc aggagtccag ccgtccagcc tcgggggtgta ggtttctgag 1980
gtgtgccatt ggggcctcag ccttctctgg tgacagaggc tcagctgtgg ccaccaacac 2040
acaaccacac acacacaacc acacacacaa atgggggcaa ccacatccag tacaagcttt 2100
tacaatggtt attagtgtcc ttttttattt ctaatgcctt gtcctcttaa aagttatttt 2160
atttgttatt attatttgtt cttgactgtt aattgtgaat ggtaatgcaa taaagtgcct 2220
ttgttagatg gtgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2263

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(2) INFORMATION ON SEQ ID NO. 81:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```

aaaaatgggc taaactagct ccagagaact tgtgaattct ttgctaaagc ctctggcaaa 60
aacggcattt gatgaagcaa ttgctgaatt ggatacgctg aatgaagagt cttataaaga 120
cagcactctg atcatgcagt tacttaggga caatctcact ctgtggacat cggaaaacca 180
gggagacgaa ggagacgctg gggagggaga gaactaatgt ttctcgtgct ttgtgatctg 240
ttcagtggtca ctctgtaccc tcaacatata tccttgtgct gataaaaaaa aaaaaaaaaa 300
aaaaaagagt cgtacgtcga ctttcgattt ttcacagcct cagcctagga aaaaatgggtc 360
atgggataaa cagctggtat ttgtatctaa aactcagatt ggtcacataa atgccacggc 420
attccgaagt tttgattttg attaacattg acaggattac tgtgtgttta attttttaa 480
aactgaacac tgtgattatg gggttttgta atttagcaga actcttactg gtagaaaaaa 540
tagacctgaa ttatgtgtaa ctttttggaa ggtttaatct gatatcaaaa taatcattga 600
aatacaattc cattgtaaag ttgtacagaa agttatagag attatattgt gatgctggaa 660
cttggagtga gacacacatc atttggcatt tgagttgaat ggtaattcac agtaatgctg 720
ccgttggttcg ggacttaaaag acacttgacc tgtttgggct gttgccactt aaaagttcat 780
gaccacaaat gtccacagtg tcttcctctg aggaactcg aatcctgaaa tggaaattct 840
ttgtggcaga taactggctt atgacacctt gaaaagttca agtgctcata taacacacca 900
cactgaaccc cctttcctac agcaatatgt tcactatgtt accaatttgc aacttgtgct 960
tcaatagtgg aatctacttt cattgttaac actgagctaa agaaaaaaag ccgtgtgttt1020
tatgaatgac cttatctgtt tcttgataa tacctttaag aataatgtcc tgagtcaggc1080
gtggtggtgc gtgcatctag tcccaactat ttgggaggct gaggcaggag gatcgcttgall140
gccaggagt ttaaagctgc agtgccctgt ggttgacact gtgaataact gactccagc1200
ctgggcaaca tagcgagacc tcatctccaa aaaagaaaaa aacacaaaag gatgtgtctg1260
taagaggctt ccctggggga ccag
1284

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(2) INFORMATION ON SEQ ID NO. 82:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1335 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

gggtgacata atgacaggtt aaatatttgt gattcattga tttaaataatta tttaaagaaa 60
tgtaaaattca caataagggg tgaaaattat ttgggtttcat ccattgtctc ttatttcagg 120
accaagcagc aaactgcagt agttttgtgaa ggattccta atgggggttca ggaatagcct 180
ctcaacgcta ctaattcaga tctctcccag agaactactg gatttcctca taattgacaa 240
acatgagtga ccacctcttt gggtggctac tgtagaagaa ggctgtgtgc atgttttctg 300
gactttgcca gccaacagat ccctgccagg ttttggaat acttctatta cctcgtgct 360
acttttctgc agggataaaa cttttgaggt ggccagacc agaacatcca aggattcctg 420
ttacagtgtc acagtataca ctgctcattt atcctattct catgtgcttt cttctttagt 480
aagattattt taagaaaata agtgatattt aaagtccaaa gaggaatgat cacagttgta 540
taaggggtgt tttcccactt gaactctgat gtcagtcgac tgtgggtcag agctacaacc 600
atctgtttgg tttgatgttt tgggtggtta cttacggagt ggggatagtg tgagacctaa 660
ttccctgtgc aaatgtctct tattccagaa atgtgcattt tgtcatctat aagcaagaaa 720
tatgggcata gcagctcttg gtttaaagtt tgccataacc tgttcatgtt tgttttaagc 780
tcaggtaaag ataacctcct ctttctatga ctccagtttc cattcaggtt atagtattat 840
tcaatagttg attttctttt taagctgggc aataaattga tgtttccaga tggtaacatg 900
ggagagggca tataggataa agatgagcaa attctaccct aaaaatgttc tagtagttca 960
caggaagaag atgaggttta ataactttca aggtaattct agattgacat tttgagggga1020
aaatgggctc ttgttctagt tgaagtgagc agagaaggct ataaattaat atgtaactta1080
cagcattcca gaggttaaaa ataactgatg cagatgtact tcttcagtgt gattcttcag1140
atcaaaactt tacttttggc atagttaatt tcagaaaaat gtgctgtatg tgtgtgtgta1200
tgagggttgg tcttctgtat ccttcagtta gctctaaatt ctggcaactc cttgtaattc1260
ccatgtattt gataccatga accaatcatg ttgaatgcgt ttggtgatct ggggagcctc1320
ccccgtcttc ccagg                                     1335

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